

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:58:31 ; Search time 15.3602 Seconds
(without alignments)
10767.297 Million cell updates/sec

Title: US-10-541-346-2

Perfect score: 20

Sequence: 1 ttgaatatattacaaagc 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19	95.0	715	4	US-09-925-065A-502888
C 2	19	95.0	819	5	US-10-027-632-166247
C 3	19	95.0	819	6	US-10-027-632-166247
4	18.4	92.0	607	4	US-09-925-065A-661036
5	18.4	92.0	647	4	US-09-925-065A-665667
C 6	18.4	92.0	8553	7	US-10-613-053A-1
C 7	18.4	92.0	8553	7	US-10-451-366A-1
8	18.4	92.0	180216	3	US-09-835-232-6
9	18.4	92.0	180216	6	US-10-308-485-6
10	18.4	92.0	271990	6	US-10-195-144-87
11	18.4	92.0	271990	6	US-10-345-072-87
C 12	18	90.0	372	4	US-09-925-065A-199410
C 13	18	90.0	372	4	US-09-925-065A-199411
14	18	90.0	844	5	US-10-027-632-155478
15	18	90.0	844	6	US-10-027-632-155478
C 16	18	90.0	4320	7	US-10-630-518-17
17	18	90.0	4320	7	US-10-630-518-21
C 18	17.4	87.0	546	4	US-09-925-065A-97366
C 19	17.4	87.0	562	4	US-09-925-065A-853310
C 20	17.4	87.0	596	4	US-09-925-065A-601207
C 21	17.4	87.0	596	4	US-09-925-065A-601208
22	17.4	87.0	226215	5	US-10-087-192-1948
23	16.8	84.0	211	4	US-09-925-065A-192206

24	16.8	84.0	211	4	US-09-925-065A-192207	Sequence 192207,
C 25	16.8	84.0	214	9	US-10-926-683-63	Sequence 63, Appl
C 26	16.8	84.0	352	4	US-09-925-065A-371009	Sequence 371009,
C 27	16.8	84.0	368	4	US-09-925-065A-580465	Sequence 580465,
28	16.8	84.0	417	4	US-09-925-065A-642312	Sequence 642312,
29	16.8	84.0	417	4	US-09-925-065A-642314	Sequence 642314,
30	16.8	84.0	417	4	US-09-925-065A-642315	Sequence 642315,
31	16.8	84.0	417	4	US-09-925-065A-642316	Sequence 642316,
32	16.8	84.0	458	4	US-09-925-065A-747766	Sequence 747766,
33	16.8	84.0	468	5	US-10-027-632-92083	Sequence 92083, A
34	16.8	84.0	468	5	US-10-027-632-317894	Sequence 317894,
35	16.8	84.0	468	6	US-10-027-632-92083	Sequence 92083, A
36	16.8	84.0	468	6	US-10-027-632-317894	Sequence 317894,
C 37	16.8	84.0	476	4	US-09-925-065A-797645	Sequence 797645,
38	16.8	84.0	478	7	US-10-242-535A-38621	Sequence 38621, A
39	16.8	84.0	478	7	US-10-085-783A-38621	Sequence 38621, A
C 40	16.8	84.0	479	4	US-09-925-065A-635386	Sequence 635386,
41	16.8	84.0	502	4	US-09-925-065A-222608	Sequence 222608,
42	16.8	84.0	507	4	US-09-925-065A-203071	Sequence 203071,
43	16.8	84.0	507	4	US-09-925-065A-585834	Sequence 585834,
44	16.8	84.0	507	4	US-09-925-065A-585836	Sequence 585836,
45	16.8	84.0	535	4	US-09-925-065A-149328	Sequence 149328,

ALIGNMENTS

RESULT 1

US-09-925-065A-502888/c
; Sequence 502888, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIORITY FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502888
; LENGTH: 715
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-502888

Query Match 95.0%; Score 19; DB 4; Length 715;
Best Local Similarity 100.0%; Pred. No. 6.2e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATATATTACAAAG 19
|||||
DB 441 TTGAATATATTACAAAG 423

RESULT 2

US-10-027-632-166247/c
; Sequence 166247, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome

```
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166247
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-166247

Query Match          95.0%; Score 19; DB 5; Length 819;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAG 19
    |||||
Db 441 TTGAATATATATTACAAAG 423

RESULT 3
US-10-027-632-166247/c
; Sequence 166247, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166247
; LENGTH: 819
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-166247

Query Match          95.0%; Score 19; DB 6; Length 819;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAG 19
    |||||
```

```
Db 441 TTGAATATATATTACAAAG 423

RESULT 4
US-09-925-065A-661036
; Sequence 661036, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 661036
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-661036

Query Match          92.0%; Score 18.4; DB 4; Length 607;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAG 20
    |||||
Db 383 TTGAATATATATTACAAAG 402

RESULT 5
US-09-925-065A-665667
; Sequence 665667, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 665667
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-665667

Query Match          92.0%; Score 18.4; DB 4; Length 647;
Best Local Similarity 95.0%; Pred. No. 1.1e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 TTGAATATATATTACAAAGC 20
||||| |||||||
Db 317 TTGAAATATATATTACAAAGC 336

RESULT 6
US-10-613-053A-1/c
; Sequence 1, Application US/10613053A
; Publication No. US20040088749A1
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Jun
; APPLICANT: YANAGIDATE, Ritsuko
; APPLICANT: SAKAI, Takako
; APPLICANT: FUJIMOTO, Hideya
; APPLICANT: KOIZUKA, Nobuya
; APPLICANT: HAYAKAWA, Takahiko
; TITLE OF INVENTION: A Protein Which is Involved in Recovery of Cytoplasm Male
; TITLE OF INVENTION: Fertility from Sterility and a Gene Encoding the Protein
; FILE REFERENCE: P23889
; CURRENT APPLICATION NUMBER: US/10/613.053A
; CURRENT FILING DATE: 2003-07-07
; PRIOR APPLICATION NUMBER: PCT JP02/04092
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 8553
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-10-613-053A-1

Query Match 92.0%; Score 18.4; DB 7; Length 8553;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
||||| |||||||
Db 4150 TTGAATATATATTACAAAGC 4131

RESULT 7
US-10-451-366A-1/c
; Sequence 1, Application US/10451366A
; Publication No. US20040117868A1
; GENERAL INFORMATION:
; APPLICANT: IMAMURA, Jun
; APPLICANT: YANAGIDATE, Ritsuko
; APPLICANT: SAKAI, Takako
; APPLICANT: FUJIMOTO, Hideya
; APPLICANT: KOIZUKA, Nobuya
; APPLICANT: HAYAKAWA, Takahiko
; TITLE OF INVENTION: A Protein Which is Involved in Recovery of Cytoplasm Male
; TITLE OF INVENTION: Fertility from Sterility and a Gene Encoding the Protein
; FILE REFERENCE: P23888
; CURRENT APPLICATION NUMBER: US/10/451.366A
; CURRENT FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT JP02/04092
; PRIOR FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1
; LENGTH: 8553
; TYPE: DNA
; ORGANISM: Raphanus sativus
US-10-451-366A-1

Query Match 92.0%; Score 18.4; DB 7; Length 8553;
Best Local Similarity 95.0%; Pred. No. 1.3e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
||||| |||||||

Db 4150 TTGAATATATATTACAAAGC 4131

RESULT 8
US-09-835-232-6
; Sequence 6, Application US/09835232
; Patent No. US20020098489A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/09/835,232
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-09-835-232-6

Query Match 92.0%; Score 18.4; DB 3; Length 180216;
Best Local Similarity 95.0%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
||||| |||||||
Db 56172 TTGAAATATATATTACAAAGC 56191

RESULT 9
US-10-308-485-6
; Sequence 6, Application US/10308485
; Publication No. US20030170683A1
; GENERAL INFORMATION:
; APPLICANT: Leder, Philip
; APPLICANT: Leader, Benjamin
; TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 00383/052002
; CURRENT APPLICATION NUMBER: US/10/308,485
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/835,232
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 60/196,811
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 180216
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (1)...(180216)
; OTHER INFORMATION: n = A,T,C or G
US-10-308-485-6

Query Match 92.0%; Score 18.4; DB 6; Length 180216;
Best Local Similarity 95.0%; Pred. No. 1.5e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
||||| |||||||
Db 56172 TTGAAATATATATTACAAAGC 56191

```
RESULT 10
US-10-195-144-87
; Sequence 87, Application US/10195144
; Publication No. US20030126646A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; FILE REFERENCE: 16313-0136
; CURRENT APPLICATION NUMBER: US/10/195,144
; CURRENT FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 87
; LENGTH: 271990
; TYPE: DNA
; ORGANISM: Raphanus sativum
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (144241)..(144300)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-195-144-87

Query Match          92.0%; Score 18.4; DB 6; Length 271990;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
Db 170571 TTGAATATATATTAAAAAGC 170590

RESULT 11
US-10-345-072-87
; Sequence 87, Application US/10345072
; Publication No. US20030237112A1
; GENERAL INFORMATION:
; APPLICANT: BROWN, GREGORY G.
; APPLICANT: FORMANOVA, NATASA
; APPLICANT: DENDY, CHARLES
; APPLICANT: LANDRY, BENOIT S.
; APPLICANT: CHEUNG, WING
; APPLICANT: JIN, HUA
; APPLICANT: LAI, FANG MING
; APPLICANT: LEFOREST, MARTIN
; TITLE OF INVENTION: NUCLEAR FERTILITY RESTORER GENES AND METHODS OF USE IN
; FILE REFERENCE: 16313-0210
; CURRENT APPLICATION NUMBER: US/10/345,072
; PRIOR APPLICATION NUMBER: PCT/US02/22217
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: 60/305,026
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/305,363
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: 60/308,736
; PRIOR FILING DATE: 2001-07-30
; NUMBER OF SEQ ID NOS: 179
; SOFTWARE: PatentIn Ver. 2.1
US-10-345-072-87

Query Match          92.0%; Score 18.4; DB 6; Length 271990;
Best Local Similarity 95.0%; Pred. No. 1.6e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
Db 170571 TTGAATATATATTAAAAAGC 170590

RESULT 12
US-09-925-065A-199410/c
; Sequence 199410, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199410
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199410

Query Match          90.0%; Score 18; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GAATATATATTACAAAGC 20
Db 205 GAATATATATTACAAAGC 188

RESULT 13
US-09-925-065A-199411/c
; Sequence 199411, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
```

```
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199411
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199411

Query Match          90.0%; Score 18; DB 4; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188
      |||||
      |||||

RESULT 14
US-10-027-632-155478
; Sequence 155478, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155478
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-155478

Query Match          90.0%; Score 18; DB 5; Length 844;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGAATATATATTACAAA 18
Db      827 TTGAATATATATTACAAA 844
      |||||
      |||||

RESULT 15
US-10-027-632-155478
; Sequence 155478, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
```

```
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 155478
; LENGTH: 844
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-155478

Query Match          90.0%; Score 18; DB 6; Length 844;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TTGAATATATATTACAAA 18
Db      827 TTGAATATATATTACAAA 844
      |||||
      |||||

Search completed: March 31, 2006, 07:57:48
Job time : 17.3602 secs
```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 07:14:39 ; Search time 11.0903 Seconds
(without alignments)
7200.876 Million cell updates/sec

Title: US-10-541-346-2

Perfect score: 20

Sequence: 1 ttgaatatattacaaagc 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 9263891 seqs, 1996499642 residues

Total number of hits satisfying chosen parameters: 18527782

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA New:*

- 1: /SID55/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 2: /SID55/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 3: /SID55/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 4: /SID55/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 5: /SID55/ptodata/2/pubpna/US03_NEW_PUB.seq.*
- 6: /SID55/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 7: /SID55/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 8: /SID55/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 9: /SID55/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 10: /SID55/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 11: /SID55/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 12: /SID55/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 13: /SID55/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 14: /SID55/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 15: /SID55/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	US-10-541-346-2	Sequence 2, Appli
2	20	100.0	1675	US-10-541-346-4	Sequence 4, Appli
C 3	19	95.0	715	US-09-925-065A-502888	Sequence 502888,
4	18.4	92.0	607	US-09-925-065A-661036	Sequence 661036,
5	18.4	92.0	647	US-09-925-065A-665667	Sequence 665667,
C 6	18.4	92.0	789	US-10-301-480-607861	Sequence 607861,
C 7	18.4	92.0	789	US-10-301-480-1221270	Sequence 1221270,
C 8	18	90.0	369	US-10-301-480-288106	Sequence 288106,
C 9	18	90.0	369	US-10-301-480-288107	Sequence 288107,
C 10	18	90.0	369	US-10-301-480-901515	Sequence 901515,
C 11	18	90.0	369	US-10-301-480-901516	Sequence 901516,
C 12	18	90.0	372	US-09-925-065A-199410	Sequence 199410,
C 13	18	90.0	372	US-09-925-065A-199411	Sequence 199411,
C 14	17.4	87.0	546	US-09-925-065A-97366	Sequence 97366, A
C 15	17.4	87.0	553	US-10-301-480-198305	Sequence 198305,
C 16	17.4	87.0	553	US-10-301-480-811714	Sequence 811714,
C 17	17.4	87.0	562	US-09-925-065A-853310	Sequence 853310,
18	17.4	87.0	595	US-10-301-480-552100	Sequence 552100,

19	17.4	87.0	595	10	US-10-301-480-1165509	Sequence 1165509,
C 20	17.4	87.0	596	6	US-09-925-065A-601207	Sequence 601207,
C 21	17.4	87.0	596	6	US-09-925-065A-601208	Sequence 601208,
22	17.4	87.0	1294	8	US-10-750-185-39609	Sequence 39609, A
23	17.4	87.0	1294	8	US-10-750-623-39609	Sequence 39609, A
24	17.4	87.0	1400	14	US-11-136-527-6745	Sequence 6745, A
25	17.4	87.0	1653	14	US-11-136-527-2649	Sequence 2649, Ap
C 26	17.4	87.0	2866	8	US-10-750-185-60916	Sequence 60916, A
C 27	17.4	87.0	2866	8	US-10-750-623-60916	Sequence 60916, A
28	17.4	87.0	162289	14	US-11-121-086-20	Sequence 20, Appl
C 29	17.4	87.0	165627	14	US-11-121-086-89	Sequence 89, Appl
30	16.8	84.0	211	6	US-09-925-065A-192206	Sequence 192206,
31	16.8	84.0	211	6	US-09-925-065A-192207	Sequence 192207,
32	16.8	84.0	212	10	US-10-301-480-281767	Sequence 281767,
33	16.8	84.0	212	10	US-10-301-480-895176	Sequence 895176,
C 34	16.8	84.0	218	10	US-10-301-480-281768	Sequence 281768,
C 35	16.8	84.0	218	10	US-10-301-480-895177	Sequence 895177,
C 36	16.8	84.0	351	10	US-10-301-480-441022	Sequence 441022,
C 37	16.8	84.0	351	10	US-10-301-480-1054431	Sequence 1054431,
C 38	16.8	84.0	352	6	US-09-925-065A-371009	Sequence 371009,
C 39	16.8	84.0	368	6	US-09-925-065A-580465	Sequence 580465,
40	16.8	84.0	417	6	US-09-925-065A-642312	Sequence 642312,
41	16.8	84.0	417	6	US-09-925-065A-642314	Sequence 642314,
42	16.8	84.0	417	6	US-09-925-065A-642315	Sequence 642315,
43	16.8	84.0	417	6	US-09-925-065A-642316	Sequence 642316,
44	16.8	84.0	458	6	US-09-925-065A-747766	Sequence 747766,
C 45	16.8	84.0	476	6	US-09-925-065A-797645	Sequence 797645,

ALIGNMENTS

RESULT 1

US-10-541-346-2

; Sequence 2, Application US/10541346

; Publication No. US20060059590A1

; GENERAL INFORMATION:

; APPLICANT: Cerney, Eric

; APPLICANT: Duong, Can

; APPLICANT: Hart, Jesse

; APPLICANT: Huber, Scott

; APPLICANT: Krieb, Rachel

; APPLICANT: Listello, Jennifer

; APPLICANT: Martens, Amy

; APPLICANT: Sammons, Bernard

; TITLE OF INVENTION: Cotton Event MON 88913 and Compositions and Methods for Detection

; TITLE OF INVENTION: Thereof

; FILE REFERENCE: 11899.0239.PCUS00

; CURRENT APPLICATION NUMBER: US/10/541,346

; CURRENT FILING DATE: 2005-07-05

; PRIOR APPLICATION NUMBER: 60/447,184

; PRIOR FILING DATE: 2003-02-12

; NUMBER OF SEQ ID NOS: 28

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 20

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chimeric DNA of cotton genomic DNA and transgene insert DNA

US-10-541-346-2

Query Match 100.0%; Score 20; DB 10; Length 20;

Best Local Similarity 100.0%; Pred. No. 23;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 TTGAATATATTACAAAGC 20

|||||

Db 1 TTGAATATATTACAAAGC 20

|||||

RESULT 2

US-10-541-346-4

```

; Sequence 4, Application US/10541346
; Publication No. US20060059590A1
; GENERAL INFORMATION:
; APPLICANT: Cerney, Eric
; APPLICANT: Duong, Can
; APPLICANT: Hart, Jesse
; APPLICANT: Huber, Scott
; APPLICANT: Krieb, Rachel
; APPLICANT: Listello, Jennifer
; APPLICANT: Martens, Amy
; APPLICANT: Sammons, Bernard
; TITLE OF INVENTION: Cotton Event MON 88913 and Compositions and Methods for Detection
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 11899.0239.PCUS00
; CURRENT APPLICATION NUMBER: US/10/541,346
; CURRENT FILING DATE: 2005-07-05
; PRIOR APPLICATION NUMBER: 60/447,184
; PRIOR FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 1675
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric DNA of cotton genomic DNA and transgene insert DNA
US-10-541-346-4

Query Match          100.0%; Score 20; DB 10; Length 1675;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20
    |||||
Db 589 TTGAATATATATTACAAAGC 608

RESULT 3
US-09-925-065A-502888/c
; Sequence 502888, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 502888
; LENGTH: 715
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-502888

Query Match          95.0%; Score 19; DB 6; Length 715;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAG 19
    |||||
Db 441 TTGAATATATATTACAAAG 423

```

```

; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288106
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-288106

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAATATATATTACAAAGC 20
   |||||
Db 205 GAATATATATTACAAAGC 188

RESULT 9
US-10-301-480-288107/c
; Sequence 288107, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288107
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-288107

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GAATATATATTACAAAGC 20
   |||||
Db 205 GAATATATATTACAAAGC 188

RESULT 10
US-10-301-480-901515/c
; Sequence 901515, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288106
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-288106

Query Match          92.0%; Score 18.4; DB 10; Length 789;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAGC 20
   |||||
Db 51 TTGAATATATATTACAAAGC 32

RESULT 7
US-10-301-480-1221270/c
; Sequence 1221270, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1221270
; LENGTH: 789
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1221270

Query Match          92.0%; Score 18.4; DB 10; Length 789;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAGC 20
   |||||
Db 51 TTGAATATATATTACAAAGC 32

RESULT 8
US-10-301-480-288106/c
; Sequence 288106, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288106
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-288106

Query Match          92.0%; Score 18.4; DB 10; Length 789;
Best Local Similarity 95.0%; Pred. No. 2.5e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAGC 20
   |||||
Db 51 TTGAATATATATTACAAAGC 32

```

```
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901515
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-901515

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188

RESULT 11
US-10-301-480-901516/c
; Sequence 901516, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 901516
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-901516

Query Match          90.0%; Score 18; DB 10; Length 369;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188

RESULT 12
US-09-925-065A-199410/c
; Sequence 901410, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199410
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199410

Query Match          90.0%; Score 18; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188

RESULT 13
US-09-925-065A-199411/c
; Sequence 199411, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199411
; LENGTH: 372
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-199411

Query Match          90.0%; Score 18; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 GAATATATATTACAAAGC 20
Db      205 GAATATATATTACAAAGC 188

RESULT 14
US-09-925-065A-97366/c
; Sequence 97366, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; NUMBER OF SEQ ID NOS: 957086
```

; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 97366
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-97366

Query Match 87.0%; Score 17.4; DB 6; Length 546;
Best Local Similarity 94.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAATATATATTACAAAGC 20
|||||
Db 157 TGAATATATATTAAAAAGC 139

RESULT 15
US-10-301-480-198305/c
; Sequence 198305, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198305
; LENGTH: 553
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-198305

Query Match 87.0%; Score 17.4; DB 9; Length 553;
Best Local Similarity 94.7%; Pred. No. 6.3e+02;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TGAATATATATTACAAAGC 20
|||||
Db 164 TGAATATATATTAAAAAGC 146

Search completed: March 31, 2006, 07:57:17
Job time : 11.0903 secs

Query Match	22.4%	Score 646;	DB 3;	Length 1695;
Best Local Similarity	100.0%;	Pred. No. 2.7e-132;		
Matches 646; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	2235	AAITCTCAGTCCAAAGCCTCAACAAGGTACAGGTCACAGAGTCTCCAAACCATTTAGCCAAA	2294	
DB	1	AAITCTCAGTCCAAAGCCTCAACAAGGTACAGGTCACAGAGTCTCCAAACCATTTAGCCAAA	60	
QY	2295	AGCTACAGGNATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCCAGCACATGCA	2354	
DB	61	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCCAGCACATGCA	120	
QY	2355	TCATGCTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTTAGTGGGCATCT	2414	
DB	121	TCATGCTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTTAGTGGGCATCT	180	
QY	2415	TTGAAAGTAATCTTGTCAACATCGACAGCTGCGCTTGTGGGACCCAGACAAAAAGGAAT	2474	
DB	181	TTGAAAGTAATCTTGTCAACATCGACAGCTGCGCTTGTGGGACCCAGACAAAAAGGAAT	240	
QY	2475	GGTGCAGAAATTGTTAGCGGCACCTACGACAAAGCATCTTTGCCCTTTAATTGCAAAAGATAAG	2534	

Db 241 GGTGAGAAATTGTTAGCGCACCTACAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 300
QY 2535 CAGATTCTCTAGTACAGTGGGGAACAAATTAACGTGGAAGAGCTGCTCGACAGCC 2594
Db 301 CAGATTCTCTAGTACAGTGGGGAACAAATTAACGTGGAAGAGCTGCTCGACAGCC 360
QY 2595 CACTCACTAATGCGTATGACGAACGAGTGCAGCACCAACAAAGAAATTTAGCTTCAGCTCAG 2654
Db 361 CACTCACTAATGCGTATGACGAACGAGTGCAGCACCAACAAAGAAATTTAGCTTCAGCTCAG 420
QY 2655 GATTTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 2714
Db 421 GATTTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 480
QY 2715 AAATTGGTATCGCCAAACCAAGAGAACTCCATCCTCAAAGGTTTGTAAAGGAAGAAT 2774
Db 481 AAATTGGTATCGCCAAACCAAGAGAACTCCATCCTCAAAGGTTTGTAAAGGAAGAAT 540
QY 2775 TCGATATCAAGCTTGATATCGGAAGTTTCTCTCTGAGGAGGTTGCTCGTGAATGGGA 2834
Db 541 TCGATATCAAGCTTGATATCGGAAGTTTCTCTCTGAGGAGGTTGCTCGTGAATGGGA 600
QY 2835 CACATATGGTTGTTAATAAACCATTTCATTTGTCATGAGATTTT 2880
Db 601 CACATATGGTTGTTAATAAACCATTTCATTTGTCATGAGATTTT 646

RESULT 2

US-09-737-626A-28
; Sequence 28, Application US/09737626A
; Patent No. 6660911
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intro
US-09-737-626A-28

Query Match 22.4%; Score 646; DB 3; Length 1695;
Best Local Similarity 100.0%; Pred. No. 2.7e-132;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTACAGGTACAGGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAGGTACAGGTACAGGTCTCCAAACCATTTAGCCAAA 60
QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGCACATGCA 120
QY 2355 TCATGTGCTAGTAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGTGCTAGTAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAAGCAAAAAAGGAAT 2474

Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAAGCAAAAAAGGAAT 240
QY 2475 GGTGAGAAATTGTTAGCGCACCTACAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 2534
Db 241 GGTGAGAAATTGTTAGCGCACCTACAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 300
QY 2535 CAGATTCTCTAGTACAGTGGGGAACAAATAAAGTGGAAAGAGCTGCTCGACAGCC 2594
Db 301 CAGATTCTCTAGTACAGTGGGGAACAAATAAAGTGGAAAGAGCTGCTCGACAGCC 360
QY 2595 CACTCACTAATGCGTATGACGAACGAGTGCAGCACCAACAAAGAAATTTAGCTTCAGCTCAG 2654
Db 361 CACTCACTAATGCGTATGACGAACGAGTGCAGCACCAACAAAGAAATTTAGCTTCAGCTCAG 420
QY 2655 GATTTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 2714
Db 421 GATTTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 480
QY 2715 AAATTGGTATCGCCAAACCAAGAGAACTCCATCCTCAAAGGTTTGTAAAGGAAGAAT 2774
Db 481 AAATTGGTATCGCCAAACCAAGAGAACTCCATCCTCAAAGGTTTGTAAAGGAAGAAT 540
QY 2775 TCGATATCAAGCTTGATATCGGAAGTTTCTCTCTGAGGAGGTTGCTCGTGAATGGGA 2834
Db 541 TCGATATCAAGCTTGATATCGGAAGTTTCTCTCTGAGGAGGTTGCTCGTGAATGGGA 600
QY 2835 CACATATGGTTGTTAATAAACCATTTCATTTGTCATGAGATTTT 2880
Db 601 CACATATGGTTGTTAATAAACCATTTCATTTGTCATGAGATTTT 646

RESULT 3

US-10-427-169-28
; Sequence 28, Application US/10427169
; Patent No. 6919495
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanisław
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6919495el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/427,169
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intro
US-10-427-169-28

Query Match 22.4%; Score 646; DB 3; Length 1695;
Best Local Similarity 100.0%; Pred. No. 2.7e-132;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTACAGGTACAGGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAGGTACAGGTACAGGTCTCCAAACCATTTAGCCAAA 60
QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGCACATGCA 120
QY 2355 TCATGTGCTAGTAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414

Db 121 TCATGTCAGTAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCACT 180
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCAAGCAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCAAGCAAAAAGGAAT 240
QY 2475 GGTGCAGAAATTGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGTAAAG 2534
Db 241 GGTGCAGAAATTGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGTAAAG 300
QY 2535 CAGATTCCTCTAGTACAAGTGGGGAACAAATAACCTGGGAAGAGCTGTCTGCAGGCC 2594
Db 301 CAGATTCCTCTAGTACAAGTGGGGAACAAATAACCTGGGAAGAGCTGTCTGCAGGCC 360
QY 2595 CACTCACTAATGCGTATGACGAACGAGTACGACCAACCAAAAGAAATTAGCTTGAGCTCAG 2654
Db 361 CACTCACTAATGCGTATGACGAACGAGTACGACCAACCAAAAGAAATTAGCTTGAGCTCAG 420
QY 2655 GATTTAGCAGCAATTCAGATTCGGTTCAATCAACAAAGGTACGAGCCATATCACTTTATTC 2714
Db 421 GATTTAGCAGCAATTCAGATTCGGTTCAATCAACAAAGGTACGAGCCATATCACTTTATTC 480
QY 2715 AAATTGGTATCGCCAAAACCAAGAGAACTCCATCCTCAAAAGTTTGTAGGAAGAAT 2774
Db 481 AAATTGGTATCGCCAAAACCAAGAGAACTCCATCCTCAAAAGTTTGTAGGAAGAAT 540
QY 2775 TCGATATCAAGCTTGATATCGGAAGTTCTCTCTTCAGGAGGTTCTCGTGGAAATGGGA 2834
Db 541 TCGATATCAAGCTTGATATCGGAAGTTCTCTCTTCAGGAGGTTCTCGTGGAAATGGGA 600
QY 2835 CACATATGGTTGTTATAATAAACCAATTCATTCATGTCATGAGATTTT 2880
Db 601 CACATATGGTTGTTATAATAAACCAATTCATTCATGTCATGAGATTTT 646

RESULT 4
US-10-427-180-28
; Sequence 28, Application US/10427180
; Patent No. 6949696
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6949696el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/427,180
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n = a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EF1 polynucleotides + EF1 intro
US-10-427-180-28

Query Match 22.4%; Score 646; DB 3; Length 1695;
Best Local Similarity 100.0%; Pred. No. 2,7e-132;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2235 AATTCTCAGTCCAAAGCCTCAACAAAGGTGAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAAAGGTGAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60

QY 2295 AGCTACAGAGATCAATGAAGAATCTTCAATCAAAAGTAAATCTCTGTTCCAGCACATGCA 2354
Db 61 AGCTACAGAGATCAATGAAGAATCTTCAATCAAAAGTAAATCTCTGTTCCAGCACATGCA 120
QY 2355 TCATGGTCAGTAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCACTCT 2414
Db 121 TCATGGTCAGTAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCACTCT 180
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCAAGCAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCAAGCAAAAAGGAAT 240
QY 2475 GGTGCAGAAATTGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGTAAAG 2534
Db 241 GGTGCAGAAATTGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGTAAAG 300
QY 2535 CAGATTCCTCTAGTACAAGTGGGGAACAAATAACCTGGGAAGAGCTGTCTGCAGGCC 2594
Db 301 CAGATTCCTCTAGTACAAGTGGGGAACAAATAACCTGGGAAGAGCTGTCTGCAGGCC 360
QY 2595 CACTCACTAATGCGTATGACGAACGAGTACGACCAACCAAAAGAAATTAGCTTGAGCTCAG 2654
Db 361 CACTCACTAATGCGTATGACGAACGAGTACGACCAACCAAAAGAAATTAGCTTGAGCTCAG 420
QY 2655 GATTTAGCAGCAATTCAGATTCGGTTCAATCAACAAAGGTACGAGCCATATCACTTTATTC 2714
Db 421 GATTTAGCAGCAATTCAGATTCGGTTCAATCAACAAAGGTACGAGCCATATCACTTTATTC 480
QY 2715 AAATTGGTATCGCCAAAACCAAGAGAACTCCATCCTCAAAAGTTTGTAGGAAGAAT 2774
Db 481 AAATTGGTATCGCCAAAACCAAGAGAACTCCATCCTCAAAAGTTTGTAGGAAGAAT 540
QY 2775 TCGATATCAAGCTTGATATCGGAAGTTCTCTCTTCAGGAGGTTCTCGTGGAAATGGGA 2834
Db 541 TCGATATCAAGCTTGATATCGGAAGTTCTCTCTTCAGGAGGTTCTCGTGGAAATGGGA 600
QY 2835 CACATATGGTTGTTATAATAAACCAATTCATTCATGTCATGAGATTTT 2880
Db 601 CACATATGGTTGTTATAATAAACCAATTCATTCATGTCATGAGATTTT 646

RESULT 5

US-09-737-698B-27
; Sequence 27, Application US/09737698B
; Patent No. 6462258
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6462258el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)C
; CURRENT APPLICATION NUMBER: US/09/737,698B
; CURRENT FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: US 60/171,173
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides + Act11
US-09-737-698B-27

Query Match 19.0%; Score 548; DB 3; Length 1946;
Best Local Similarity 100.0%; Pred. No. 9.4e-111;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2235 AATTCTCAGTCCAAAGCCTCAACAAAGGTGAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAAAGGTGAGGTACAGAGTCTCCAAACCATTTAGCCAAA 111

```
Db 1 AATTCTCAGTCCAAAGCCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60
QY 2295 AGCTACAGGAGATCAATGAAGAACTCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGAACTCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 120
QY 2355 TCATGGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCCAGACAAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCCAGACAAAAAAGGAAT 240
QY 2475 GGTGCAGAAATGTTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 2534
Db 241 GGTGCAGAAATGTTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 300
QY 2535 CAGATTCTCTAGTACAAGTGGGGAACAAAATAAAGTGGAAAGAGCTGTCTCGACAGCC 2594
Db 301 CAGATTCTCTAGTACAAGTGGGGAACAAAATAAAGTGGAAAGAGCTGTCTCGACAGCC 360
QY 2595 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACAAAAGAAATTTAGCTTGAGCTCAG 2654
Db 361 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACAAAAGAAATTTAGCTTGAGCTCAG 420
QY 2655 GATTTAGCAGCATTCAGATTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTTC 2714
Db 421 GATTTAGCAGCATTCAGATTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTTC 480
QY 2715 AAATTGGTATCGCCAAAACCAAGAAGAACTCCCATCTCTCAAAAGTTTGTGAAGGAAGAAT 2774
Db 481 AAATTGGTATCGCCAAAACCAAGAAGAACTCCCATCTCTCAAAAGTTTGTGAAGGAAGAAT 2774
QY 2775 TCGATATC 2782
Db 541 TCGATATC 548

RESULT 6
US-09-737-626A-27
; Sequence 27, Application US/09737626A
; Patent No. 6660911
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flaszinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6660911el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/09/737,626A
; CURRENT FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +
; OTHER INFORMATION: ntro
US-09-737-626A-27

Query Match 19.0%; Score 548; DB 3; Length 1946;
Best Local Similarity 100.0%; Pred.No. 9.4e-111; Indels 0; Gaps 0;
Matches 548; Conservative 0; Mismatches 0;

QY 2235 AATTCTCAGTCCAAAGCCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60
```

```
QY 2295 AGCTACAGGAGATCAATGAAGAACTCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGAACTCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 120
QY 2355 TCATGGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCAGTAAGTTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCCAGACAAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCCAGACAAAAAAGGAAT 240
QY 2475 GGTGCAGAAATGTTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 2534
Db 241 GGTGCAGAAATGTTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTATTGCAAGATAAAG 300
QY 2535 CAGATTCTCTAGTACAAGTGGGGAACAAAATAAAGTGGAAAGAGCTGTCTCGACAGCC 2594
Db 301 CAGATTCTCTAGTACAAGTGGGGAACAAAATAAAGTGGAAAGAGCTGTCTCGACAGCC 360
QY 2595 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACAAAAGAAATTTAGCTTGAGCTCAG 2654
Db 361 CACTCACTAATCGGTATGACGAACGCGAGTGAACCAACAAAAGAAATTTAGCTTGAGCTCAG 420
QY 2655 GATTTAGCAGCATTCAGATTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTTC 2714
Db 421 GATTTAGCAGCATTCAGATTGGGTTCAATCAACAAGGTACGAGCCATATCACTTTATTTC 480
QY 2715 AAATTGGTATCGCCAAAACCAAGAAGAACTCCCATCTCTCAAAAGTTTGTGAAGGAAGAAT 2774
Db 481 AAATTGGTATCGCCAAAACCAAGAAGAACTCCCATCTCTCAAAAGTTTGTGAAGGAAGAAT 2774
QY 2775 TCGATATC 2782
Db 541 TCGATATC 548

RESULT 7
US-10-427-169-27
; Sequence 27, Application US/10427169
; Patent No. 6919495
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flaszinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6919495el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/427,169
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +
; OTHER INFORMATION: ntro
US-10-427-169-27

Query Match 19.0%; Score 548; DB 3; Length 1946;
Best Local Similarity 100.0%; Pred.No. 9.4e-111; Indels 0; Gaps 0;
Matches 548; Conservative 0; Mismatches 0;

QY 2235 AATTCTCAGTCCAAAGCCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60
```

Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTGAGGTCAGAGTCTCCAAACCATTTAGCCAAA 60
QY 2295 AGCTACAGGAGATCAATGAGAACTCTTCAATCAAGTAAGTAACTCTTCCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAGAACTCTTCAATCAAGTAAGTAACTCTTCCAGCACATGCA 120
QY 2355 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTTAAAGTTAGTGGGCATCT 180
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAAAAGGAAT 240
QY 2475 GGTGCGAAGTTGTTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAG 2534
Db 241 GGTGCGAAGTTGTTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAG 300
QY 2535 CAGATTCTCTAGTACAGTGGGGACCAAAATAACGTGGAAAGAGCTGCTCCTGACAGCC 2594
Db 301 CAGATTCTCTAGTACAGTGGGGACCAAAATAACGTGGAAAGAGCTGCTCCTGACAGCC 360
QY 2595 CACTCACTAATCGTATGACGAACGCGAGTACGACCAACAAAGAAATTTAGCTTCAGGCTCAG 2654
Db 361 CACTCACTAATCGTATGACGAACGCGAGTACGACCAACAAAGAAATTTAGCTTCAGGCTCAG 420
QY 2655 GATTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 2714
Db 421 GATTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 480
QY 2715 AAATTGGTATCGCCAAAACCAAGAGAACTCCCATCTCCAAAGGTTTGTGAAGGAAGAAT 2774
Db 481 AAATTGGTATCGCCAAAACCAAGAGAACTCCCATCTCCAAAGGTTTGTGAAGGAAGAAT 540
QY 2775 TCGATATC 2782
Db 541 TCGATATC 548

RESULT 8
US-10-427-180-27
; Sequence 27, Application US/10427180
; Patent No. 6949696
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiński, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. 6949696el Plant Expression Constructs
; FILE REFERENCE: 38-21(514991B)
; CURRENT APPLICATION NUMBER: US/10/427,180
; CURRENT FILING DATE: 2003-05-01
; PRIOR APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides + Act11
; OTHER INFORMATION: ntro
US-10-427-180-27

Query Match 19.0%; Score 548; DB 3; Length 1946;
Best Local Similarity 100.0%; Pred. No. 9.4e-111;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2235 AATTCTCAGTCCAAAGCCTCAACAAGGTGAGGTCAGAGTCTCCAAACCATTTAGCCAAA 2294

Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTGAGGTCAGAGTCTCCAAACCATTTAGCCAAA 60
QY 2295 AGCTACAGGAGATCAATGAGAACTCTTCAATCAAGTAAGTAACTCTTCCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAGAACTCTTCAATCAAGTAAGTAACTCTTCCAGCACATGCA 120
QY 2355 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTTAAAGTTAGTGGGCATCT 180
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAAAAGGAAT 240
QY 2475 GGTGCGAAGTTGTTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAG 2534
Db 241 GGTGCGAAGTTGTTAGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTTGCAAAAGATAAG 300
QY 2535 CAGATTCTCTAGTACAGTGGGGACCAAAATAACGTGGAAAGAGCTGCTCCTGACAGCC 2594
Db 301 CAGATTCTCTAGTACAGTGGGGACCAAAATAACGTGGAAAGAGCTGCTCCTGACAGCC 360
QY 2595 CACTCACTAATCGTATGACGAACGCGAGTACGACCAACAAAGAAATTTAGCTTCAGGCTCAG 2654
Db 361 CACTCACTAATCGTATGACGAACGCGAGTACGACCAACAAAGAAATTTAGCTTCAGGCTCAG 420
QY 2655 GATTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 2714
Db 421 GATTAGCAGCATTCAGAGTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTC 480
QY 2715 AAATTGGTATCGCCAAAACCAAGAGAACTCCCATCTCCAAAGGTTTGTGAAGGAAGAAT 2774
Db 481 AAATTGGTATCGCCAAAACCAAGAGAACTCCCATCTCCAAAGGTTTGTGAAGGAAGAAT 540
QY 2775 TCGATATC 2782
Db 541 TCGATATC 548

RESULT 9
US-07-753-738B-6
; Sequence 6, Application US/07753738B
; Patent No. 5304730
; GENERAL INFORMATION:
; APPLICANT: Lawson, Edgar C.
; APPLICANT: Weiss, James D.
; APPLICANT: Hemenway, Cynthia L.
; APPLICANT: Turner, Nilgun E.
; TITLE OF INVENTION: Virus Resistant Plants and Method
; TITLE OF INVENTION: Therefore
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/753,738B
; FILING DATE: 19910903
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10536)A
; TELECOMMUNICATION INFORMATION:

```
;
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-753-738B-6

Query Match 14.2%; Score 409.2; DB 2; Length 597;
Best Local Similarity 98.1%; Pred. No. 2.1e-80;
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTGACAGGTGACAGGTCTCCAAACCATTAGCCAAA 2294
Db 127 AATTCTCAGTCCAAAGCCTCAACAGGTGACAGGTGACAGGTCTCCAAACCATTAGCCAAA 186

QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 2354
Db 187 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 246

QY 2355 TCATGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 247 TCATGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 306

QY 2415 TTGAAGTAATCTTGTCAACATCGACAGCTGGCTTGTGGGACCGACAGAAAAAGGAAT 2474
Db 307 TTGAAGTAATCTTGTCAACATCGACAGCTGGCTTGTGGGACCGACAGAAAAAGGAAT 366

QY 2475 GGTGCAGAAATGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGTAAAG 2534
Db 367 GGTGCAGAAATGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGTAAAG 426

QY 2535 CAGATTCTCTAGTCAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCTCTGACAGCC 2594
Db 427 CAGATTCTCTAGTCAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCTCTGACAGCC 486

QY 2595 CACTCACTAATCGGTATGACGACGACGACGACGACGACGACGACGACGACGACGACG 2654
Db 487 CACTCACTAATCGGTATGACGACGACGACGACGACGACGACGACGACGACGACGACG 546

QY 2655 GA 2656
Db 547 AA 548

RESULT 10
US-08-368-260-4
; Sequence 4, Application US/08368260
; Patent No. 5503999
; GENERAL INFORMATION:
; APPLICANT: Tumer, Nilgun E.
; APPLICANT: Jilka, Joseph M.
; TITLE OF INVENTION: Virus Resistant Plants
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle D. Strode, Monsanto Co., BB4F
; STREET: 700 Chesterfield Parkway No. 5503999th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/368,260
; FILING DATE:
; CLASSIFICATION: 800
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,416
; FILING DATE:
; APPLICATION NUMBER: US/07/910,224
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Strode, Janelle D.
; REGISTRATION NUMBER: 34,738
; REFERENCE/DOCKET NUMBER: 38-21(10550)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-368-260-4

Query Match 14.2%; Score 409.2; DB 2; Length 597;
Best Local Similarity 98.1%; Pred. No. 2.1e-80;
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTGACAGGTGACAGGTCTCCAAACCATTAGCCAAA 2294
Db 127 AATTCTCAGTCCAAAGCCTCAACAGGTGACAGGTGACAGGTCTCCAAACCATTAGCCAAA 186

QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 2354
Db 187 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCATGCA 246

QY 2355 TCATGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 247 TCATGTCAGTAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 306

QY 2415 TTGAAGTAATCTTGTCAACATCGACAGCTGGCTTGTGGGACCGACAGAAAAAGGAAT 2474
Db 307 TTGAAGTAATCTTGTCAACATCGACAGCTGGCTTGTGGGACCGACAGAAAAAGGAAT 366

QY 2475 GGTGCAGAAATGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGTAAAG 2534
Db 367 GGTGCAGAAATGTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGTAAAG 426

QY 2535 CAGATTCTCTAGTCAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCTCTGACAGCC 2594
Db 427 CAGATTCTCTAGTCAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCTCTGACAGCC 486

QY 2595 CACTCACTAATCGGTATGACGACGACGACGACGACGACGACGACGACGACGACGACG 2654
Db 487 CACTCACTAATCGGTATGACGACGACGACGACGACGACGACGACGACGACGACGACG 546

QY 2655 GA 2656
Db 547 AA 548

RESULT 11
US-07-809-457A-17
; Sequence 17, Application US/07809457A
; Patent No. 5512466
; GENERAL INFORMATION:
; APPLICANT: Klee, Harry J.
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: Control of Fruit Ripening and Senescence
; TITLE OF INVENTION: in Plants
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
```

; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/809,457A
; FILING DATE: 19911217
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/632,440
; FILING DATE: 26-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10538)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-07-809-457A-17

Query Match 14.2%; Score 409.2; DB 2; Length 597;

Best Local Similarity 98.1%; Pred. No. 2.1e-80;
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	2235	AATTCTCAGTCCAAAGCTCAACAGGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAA	2294
DB	127	AATTCTCAGTCCAAAGCTCAACAGGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAA	186
QY	2295	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA	2354
DB	187	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA	246
QY	2355	TCATGTCAGTAAGTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGCATCT	2414
DB	247	TCATGTCAGTAAGTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGCATCT	306
QY	2535	CAGATTCTCTAGTACAGTGGGAAACAAATAACGTTGGAAGAGCTGCTTGCACAGCC	2594
DB	427	CAGATTCTCTAGTACAGTGGGAAACAAATAACGTTGGAAGAGCTGCTTGCACAGCC	486
QY	2595	CACCTCACTAATGCGTATGACGAAACGCGAGTGCAGACCAACAAAGAAATTCCTCTATATAAG	2654
DB	487	CACCTCACTAATGCGTATGACGAAACGCGAGTGCAGACCAACAAAGAAATTCCTCTATATAAG	546
QY	2655	GA 2656	
DB	547	AA 548	

RESULT 12

US-08-148-022-5
; Sequence 5, Application US/08148022
; Patent No. 5589612
; GENERAL INFORMATION:
; APPLICANT: Tumer, Nilgun E.

; APPLICANT: Jilka, Joseph M.
; TITLE OF INVENTION: Virus Resistant Plants
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle D. Strode, Monsanto Co., BB4F
; STREET: 700 Chesterfield Parkway No. 5589612th
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/148,022
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/910,792
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Strode, Janelle D.
; REGISTRATION NUMBER: 34,738
; REFERENCE/DOCKET NUMBER: 38-21(10549)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6224
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-148-022-5

Query Match 14.2%; Score 409.2; DB 2; Length 597;

Best Local Similarity 98.1%; Pred. No. 2.1e-80;
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY	2235	AATTCTCAGTCCAAAGCTCAACAGGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAA	2294
DB	127	AATTCTCAGTCCAAAGCTCAACAGGTCAAGGTACAGAGTCTCCAAACCATTAGCCAAA	186
QY	2295	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA	2354
DB	187	AGCTACAGGAGATCAATGAAGAATCTTCAATCAAAAGTAAACTACTGTTCCAGCACATGCA	246
QY	2355	TCATGTCAGTAAGTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGCATCT	2414
DB	247	TCATGTCAGTAAGTTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGCATCT	306
QY	2415	TTGAAAGTAATCTTGTCAACATCGAGCGCTGGCTTGTGGGACCAACAAAGAAAT	2474
DB	307	TTGAAAGTAATCTTGTCAACATCGAGCGCTGGCTTGTGGGACCAACAAAGAAAT	366
QY	2475	GGTGCAGAAATGTTAGCGCACCTTACCAAAAGCATCTTTCGCTTATTGCAAGATAAG	2534
DB	367	GGTGCAGAAATGTTAGCGCACCTTACCAAAAGCATCTTTCGCTTATTGCAAGATAAG	426
QY	2535	CAGATTCTCTAGTACAGTGGGAAACAAATAACGTTGGAAGAGCTGCTTGCACAGCC	2594
DB	427	CAGATTCTCTAGTACAGTGGGAAACAAATAACGTTGGAAGAGCTGCTTGCACAGCC	486
QY	2595	CACCTCACTAATGCGTATGACGAAACGCGAGTGCAGACCAACAAAGAAATTCCTCTATATAAG	2654
DB	487	CACCTCACTAATGCGTATGACGAAACGCGAGTGCAGACCAACAAAGAAATTCCTCTATATAAG	546
QY	2655	GA 2656	
DB	547	AA 548	

RESULT 13
US-08-476-008-1
; Sequence 1, Application US/08476008
; Patent No. 5627061
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glyphosate Tolerant
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,008
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/306,063
; FILING DATE: 13-SEP-1994
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10660)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-476-008-1
Query Match 14.2%; Score 409.2; DB 2; Length 597;
Best Local Similarity 98.1%; Pred. No. 2.1e-80;
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTCCAGGTACAGAGTCTCCAAACATTAGCCAAA 2294
DB 127 AATTCTCAGTCCAAAGCCTCAACAGGTCCAGGTACAGAGTCTCCAAACATTAGCCAAA 186
QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAGTAAGTACTGTTCCAGCACATGCA 2354
DB 187 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAGTAAGTACTGTTCCAGCACATGCA 246
QY 2355 TCATGGTCAAGTAAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCACT 2414
DB 247 TCATGGTCAAGTAAAGTTTCAGAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCACT 306
QY 2415 TTGAAAGTAATCTTGTCACATCGAGCAGCTGGCTTGTGGGACCAGACAAAAAGGAAT 2474

DB 307 TTGAAAGTAATCTTGTCACATCGAGCAGCTGGCTTGTGGGACCAGACAAAAAGGAAT 366
QY 2475 GGTGAGAAATTTAGGCGCACCTACCAAAAGCACTTTTGGCCTTTATTGCAAGATAAAG 2534
DB 367 GGTGAGAAATTTAGGCGCACCTACCAAAAGCACTTTTGGCCTTTATTGCAAGATAAAG 426
QY 2535 CAGATTCTCTAGTACAGTGGGGACAAAAATAACGTGAAAAGAGCTCTCTGACAGCC 2594
DB 427 CAGATTCTCTAGTACAGTGGGGACAAAAATAACGTGAAAAGAGCTCTCTGACAGCC 486
QY 2595 CACTCACTAATCGGTATGACGAAACGAGTACGACCAACAAAAAGAAATTAGCTTGAAGCTCAG 2654
DB 487 CACTCACTAATCGGTATGACGAAACGAGTACGACCAACAAAAAGAAATTCCCTCTATATAAG 546
QY 2655 GA 2656
DB 547 AA 548
RESULT 14
US-08-306-063-1
; Sequence 1, Application US/08306063
; Patent No. 5633435
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: Glyphosate Tolerant
; NUMBER OF SEQUENCES: 69
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
; STREET: 700 Chesterfield Village Parkway
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63198
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/306,063
; FILING DATE: 13-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,611
; FILING DATE: 28-AUG-1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/576,537
; FILING DATE: 31-AUG-1990
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hoerner Jr., Dennis R.
; REGISTRATION NUMBER: 30,914
; REFERENCE/DOCKET NUMBER: 38-21(10660)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)537-6099
; TELEFAX: (314)537-6047
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 597 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-306-063-1
Query Match 14.2%; Score 409.2; DB 2; Length 597;

57	181	TTGAAAGTAACTTTGTCAA	CATCAGCAGCTGGCTTGTGGGGACCGAC	AAAAAGGAAT	240
----	-----	---------------------	------------------------------	------------	-----

Db 61 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAATCTAGTGTTCAGCACATGCA 120
QY 2355 TCATGGTCACTAGTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCACTAGTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180
QY 2415 TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAACAAAAAGGAAT 2474
Db 181 TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAACAAAAAGGAAT 240
QY 2475 GGTGCGAATTTGTAGCGCACCTTACCAAGCATCTTTCGCCCTTATTGCAAGATAAAG 2534
Db 241 GGTGCGAATTTGTAGCGCACCTTACCAAGCATCTTTCGCCCTTATTGCAAGATAAAG 300
QY 2535 CAGATTCTCTAGTACAAAGTGGGGAACAAAAATAACGTGGAAGAGCTGCTCTGACAGCC 2594
Db 301 CAGATTCTCTAGTACAAAGTGGGGAACAAAAATAACGTGGAAGAGCTGCTCTGACAGCC 360
QY 2595 CACTCACTAATCGTATGACGAACGCGAGTGAACCAACCAAGGATTTAGCTTGGCTCAG 2654
Db 361 CACTCACTAATCGTATGACGAACGCGAGTGAACCAACCAAGGATTTAGCTTGGCTCAG 420
QY 2655 GATTAGCAGATTCAGATTGGGTTCAATCAACAGGTACGAGCCATATCATTATTTC 2714
Db 421 GATTAGCAGATTCAGATTGGGTTCAATCAACAGGTACGAGCCATATCATTATTTC 480
QY 2715 AAATTGGTATCGCCAAACCAAGGAACCTCCATCTCCAAAGGTTTGTAAAGGAAGAT 2774
Db 481 AAATTGGTATCGCCAAACCAAGGAACCTCCATCTCCAAAGGTTTGTAAAGGAAGAT 540
QY 2775 TCGATATCAAGCTTGATATCGGAAGTTTCTCTTGGAGGAGGTTGCTCGTGGAAATGGGA 2834
Db 541 TCGATATCAAGCTTGATATCGGAAGTTTCTCTTGGAGGAGGTTGCTCGTGGAAATGGGA 600
QY 2835 CACATATGGTTGTTATTAATAAACCAATTTCCATTGTCATGAGATTTT 2880
Db 601 CACATATGGTTGTTATTAATAAACCAATTTCCATTGTCATGAGATTTT 646

RESULT 4
US-10-909-860-28
; Sequence 28, Application US/10909860
; Publication No. US2005005332A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiniski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: Novel Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/909,860
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: US/09/737,626
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EFl polynucleotides + EFl intron
US-10-909-860-28

Query Match 22.4%; Score 646; DB 8; Length 1695;
Best Local Similarity 100.0%; Pred. No. 3.9e-115;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTCAGGGTCAGAGTCTCCAAACCAATTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAGGTCAGGGTCAGAGTCTCCAAACCAATTAGCCAAA 60
QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAATCTACTGTTCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAATCTACTGTTCAGCACATGCA 120
QY 2355 TCATGGTCACTAGTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCACTAGTTCAGAAAAAGACATCCACCGAAGACTTAAAGTTAGTGGGCATCT 180
QY 2415 TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAACAAAAAGGAAT 2474
Db 181 TTGAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCAACAAAAAGGAAT 240
QY 2475 GGTGCGAATTTGTAGCGCACCTTACCAAGCATCTTTCGCCCTTATTGCAAGATAAAG 2534
Db 241 GGTGCGAATTTGTAGCGCACCTTACCAAGCATCTTTCGCCCTTATTGCAAGATAAAG 300
QY 2535 CAGATTCTCTAGTACAAAGTGGGGAACAAAAATAACGTGGAAGAGCTGCTCTGACAGCC 2594
Db 301 CAGATTCTCTAGTACAAAGTGGGGAACAAAAATAACGTGGAAGAGCTGCTCTGACAGCC 360
QY 2595 CACTCACTAATCGTATGACGAACGCGAGTGAACCAACCAAGGATTTAGCTTGGCTCAG 2654
Db 361 CACTCACTAATCGTATGACGAACGCGAGTGAACCAACCAAGGATTTAGCTTGGCTCAG 420
QY 2655 GATTAGCAGATTCAGATTGGGTTCAATCAACAGGTACGAGCCATATCATTATTTC 2714
Db 421 GATTAGCAGATTCAGATTGGGTTCAATCAACAGGTACGAGCCATATCATTATTTC 480
QY 2715 AAATTGGTATCGCCAAACCAAGGAACCTCCATCTCCAAAGGTTTGTAAAGGAAGAT 2774
Db 481 AAATTGGTATCGCCAAACCAAGGAACCTCCATCTCCAAAGGTTTGTAAAGGAAGAT 540
QY 2775 TCGATATCAAGCTTGATATCGGAAGTTTCTCTTGGAGGAGGTTGCTCGTGGAAATGGGA 2834
Db 541 TCGATATCAAGCTTGATATCGGAAGTTTCTCTTGGAGGAGGTTGCTCGTGGAAATGGGA 600
QY 2835 CACATATGGTTGTTATTAATAAACCAATTTCCATTGTCATGAGATTTT 2880
Db 601 CACATATGGTTGTTATTAATAAACCAATTTCCATTGTCATGAGATTTT 646

RESULT 5
US-10-920-869-28
; Sequence 28, Application US/10920869
; Publication No. US2005002261A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasiniski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: Novel Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/920,869
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US/09/737,626
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 28
; LENGTH: 1695
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1695)
; OTHER INFORMATION: n= a or g or c or t/u, r = g or a, y = t/u or c
; OTHER INFORMATION: chimeric promoter fusion FMV and EFl polynucleotides + EFl intron
US-10-920-869-28

Query Match 22.4%; Score 646; DB 8; Length 1695;
Best Local Similarity 100.0%; Pred. No. 3.9e-115; Mismatches 0; Indels 0; Gaps 0;
Matches 646; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTGAGGTGACAGAGTCTCCAAAGCATTAGGCCAA 2294
DB 1 AATTCTCAGTCCAAAGCCTCAACAGGTGAGGTGACAGAGTCTCCAAAGCATTAGGCCAA 60
QY 2295 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAACTACTGTTTCAGCACATGCA 2354
DB 61 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAACTACTGTTTCAGCACATGCA 120
QY 2355 TCATGTCAGTAAAGTTTCAGAAAGACATCCACCGAGCTTAAAGTTAGTGGCATCT 2414
DB 121 TCATGTCAGTAAAGTTTCAGAAAGACATCCACCGAGCTTAAAGTTAGTGGCATCT 180
QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGACAAAAAGGAAT 2474
DB 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTGTGGGACACAGACAAAAAGGAAT 240
QY 2475 GGTGCAGAAATTGTTAGGCGCCTTACCAAAAGCATCTTTGCCCTTTATTCGAAAGTAAAG 2534
DB 241 GGTGCAGAAATTGTTAGGCGCCTTACCAAAAGCATCTTTGCCCTTTATTCGAAAGTAAAG 300
QY 2535 CAGATTCCTCTAGTACAAGTGGGACCAAAATTAACGTGGAAAGAGCTGTCTGCAGCC 2594
DB 301 CAGATTCCTCTAGTACAAGTGGGACCAAAATTAACGTGGAAAGAGCTGTCTGCAGCC 360
QY 2595 CACTCACTAATCGGTATGACGAACGAGTGACGACCAACAAAGAAATTAGCTTGGCTCAG 2654
DB 361 CACTCACTAATCGGTATGACGAACGAGTGACGACCAACAAAGAAATTAGCTTGGCTCAG 420
QY 2655 GATTAGCAGATTCAGATTTGGTTTCAATCAACAGGTACGAGCCATATCATCTTTATTC 2714
DB 421 GATTAGCAGATTCAGATTTGGTTTCAATCAACAGGTACGAGCCATATCATCTTTATTC 480
QY 2715 AAATGGTATCGCCAAACCAAGAGAACTCCCATCTCCAAAGTTTGTAGGAAGAT 2774
DB 481 AAATGGTATCGCCAAACCAAGAGAACTCCCATCTCCAAAGTTTGTAGGAAGAT 540
QY 2775 TCGATATCAAGCTTGATATCGGAAGTTTCTCTTGGAGGAGGTGCTCGTGGAAATGGGA 2834
DB 541 TCGATATCAAGCTTGATATCGGAAGTTTCTCTTGGAGGAGGTGCTCGTGGAAATGGGA 600
QY 2835 CACATATGGTTGTATATAAACCATTTCATTTGTCATGAGATTTT 2880
DB 601 CACATATGGTTGTATATAAACCATTTCATTTGTCATGAGATTTT 646

RESULT 6
US-09-924-197-1
; Sequence 1, Application US/09924197
; Publication No. US20030018993A1
; GENERAL INFORMATION:
; APPLICANT: Gutterson, Neal
; APPLICANT: Oeller, Paul
; TITLE OF INVENTION: Improved Methods of Gene Silencing Using Inverted
; FILE REFERENCE: 012176-010810US
; CURRENT APPLICATION NUMBER: US/09/924,197
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/225,508
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 5822
; TYPE: DNA
; ORGANISM: Agrobacterium tumefaciens
US-09-924-197-1

Query Match 19.3%; Score 556; DB 3; Length 5822;

Best Local Similarity 99.1%; Pred. No. 2e-97; Mismatches 559; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2221 CTCGAGTGAAGCTAATTTCTAGTCCAAAGCCTCAACAGGTGACAGGTCTCCA 2280
DB 284 CTCGAGTGAAGCTAATTTCTAGTCCAAAGCCTCAACAGGTGACAGGTCTCCA 343
QY 2281 AACCAATTAGCCAAAGCTACAGGAGTCAATCAAGAACTTCAATCAAAAGTAACTACTG 2340
DB 344 AACCAATTAGCCAAAGCTACAGGAGTCAATCAAGAACTTCAATCAAAAGTAACTACTG 403
QY 2341 TTCCAGCACATGCATCATGGTCAAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAA 2400
DB 404 TTCCAGCACATGCATCATGGTCAAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTAAA 463
QY 2401 GTTAGTGGGCATCTTTGAAAAGTAACTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCA 2460
DB 464 GTTAGTGGGCATCTTTGAAAAGTAACTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCA 523
QY 2461 GACAAAAAGGAATGGTCAGAAATTTGTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTA 2520
DB 524 GACAAAAAGGAATGGTCAGAAATTTGTAGGCGCACCTACCAAAAGCATCTTTGCCCTTTA 583
QY 2521 TTGCAAAAGATAAGCAGATTCCTCTAGTACAAGTGGGAAACAAAATAACGTGGAAAGAG 2580
DB 584 TTGCAAAAGATAAGCAGATTCCTCTAGTACAAGTGGGAAACAAAATAACGTGGAAAGAG 643
QY 2581 CTGTCTCGACAGCCCACTCACTAATGCGGTATGCGAAACGAGTACGACCAAAAAGAAAT 2640
DB 644 CTGTCTCGACAGCCCACTCACTAATGCGGTATGCGAAACGAGTACGACCAAAAAGAAAT 703
QY 2641 TAGCTTGAGCTCAGGATTTAGCAGCATTTCCAGATTTGGGTTTCAATCAAGAGTACGAGCC 2700
DB 704 TAGCTTGAGCTCAGGATTTAGCAGCATTTCCAGATTTGGGTTTCAATCAAGAGTACGAGCC 763
QY 2701 ATATCACTTTATTCAAATTTGGTATCGCAAAACCAAGAAAGAACTCCCATCTCTCAAAGGT 2760
DB 764 ATATCACTTTATTCAAATTTGGTATCGCAAAACCAAGAAAGAACTCCCATCTCTCAAAGGT 823
QY 2761 TTGTAAGGAAGAAATTCGATATCAA 2784
DB 824 TTGTAAGGAAGAAATTCGATATCAA 847

RESULT 7
US-09-737-626A-27
; Sequence 27, Application US/09737626A
; Patent No. US20020144304A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flisinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: No. US20020144304A1el Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/09/737,626A
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: 09/737,626
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)-(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides + Act11
US-09-737-626A-27

Query Match 19.0%; Score 548; DB 3; Length 1946;
Best Local Similarity 100.0%; Pred. No. 4.5e-96;


```
Query Match      19.0%; Score 548; DB 6; Length 1946;
Best Local Similarity 100.0%; Pred. No. 4.5e-96;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60

QY 2295 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTCTTCCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTCTTCCAGCACATGCA 120

QY 2355 TCATGGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 180

QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCAAGAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCAAGAAAAAGGAAT 240

QY 2475 GGTGCAGAAATGTTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTTCGAAAGATAAAG 2534
Db 241 GGTGCAGAAATGTTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTTCGAAAGATAAAG 300

QY 2535 CAGATTCCCTTAGTCAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCTCTGACAGCC 2594
Db 301 CAGATTCCCTTAGTCAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCTCTGACAGCC 360

QY 2595 CACTCACTAATCGGTATGACGAACGCGAGTGAACGACCAACAAAAGAAATTTAGCTTGAAGCTCAG 2654
Db 361 CACTCACTAATCGGTATGACGAACGCGAGTGAACGACCAACAAAAGAAATTTAGCTTGAAGCTCAG 420

QY 2655 GATTTAGCAGCATTCAGATTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTTC 2714
Db 421 GATTTAGCAGCATTCAGATTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTTC 480

QY 2715 AAATTGGTATCGCAAAACCAAGAAGAACTCCCATCTCTCAAAGGTTTGTGAAGGAAGAAT 2774
Db 481 AAATTGGTATCGCAAAACCAAGAAGAACTCCCATCTCTCAAAGGTTTGTGAAGGAAGAAT 540

QY 2775 TCGATATC 2782
Db 541 TCGATATC 548

RESULT 10
US-10-909-860-27
; Sequence 27, Application US/10909860
; Publication No. US20050005332A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: Novel Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/909,860
; CURRENT FILING DATE: 2004-08-02
; PRIOR APPLICATION NUMBER: US/09/737,626
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +
; OTHER INFORMATION: ntro
US-10-909-860-27
```

```
Query Match      19.0%; Score 548; DB 8; Length 1946;
Best Local Similarity 100.0%; Pred. No. 4.5e-96;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 2294
Db 1 AATTCTCAGTCCAAAGCCTCAACAAGGTCAAGGTACAGAGTCTCCAAACCATTTAGCCAAA 60

QY 2295 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTCTTCCAGCACATGCA 2354
Db 61 AGCTACAGGAGATCAATGAAGATCTTCAATCAAGTAAACTACTCTTCCAGCACATGCA 120

QY 2355 TCATGGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 2414
Db 121 TCATGGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT 180

QY 2415 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCAAGAAAAAGGAAT 2474
Db 181 TTGAAAGTAATCTTGTCAACATCGAGCAGCTGGCTTTGTGGGACCAAGAAAAAGGAAT 240

QY 2475 GGTGCAGAAATGTTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTTCGAAAGATAAAG 2534
Db 241 GGTGCAGAAATGTTTAGGCGCACCCTACCAAAAGCATCTTTGCCCTTTATTTCGAAAGATAAAG 300

QY 2535 CAGATTCCCTTAGTCAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCTCTGACAGCC 2594
Db 301 CAGATTCCCTTAGTCAAGTGGGGAACAAAATAACGTGGAAGAGCTGTCTCTGACAGCC 360

QY 2595 CACTCACTAATCGGTATGACGAACGCGAGTGAACGACCAACAAAAGAAATTTAGCTTGAAGCTCAG 2654
Db 361 CACTCACTAATCGGTATGACGAACGCGAGTGAACGACCAACAAAAGAAATTTAGCTTGAAGCTCAG 420

QY 2655 GATTTAGCAGCATTCAGATTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTTC 2714
Db 421 GATTTAGCAGCATTCAGATTTGGGTTCAATCAACAGGTACGAGCCATATCACTTTATTTC 480

QY 2715 AAATTGGTATCGCAAAACCAAGAAGAACTCCCATCTCTCAAAGGTTTGTGAAGGAAGAAT 2774
Db 481 AAATTGGTATCGCAAAACCAAGAAGAACTCCCATCTCTCAAAGGTTTGTGAAGGAAGAAT 540

QY 2775 TCGATATC 2782
Db 541 TCGATATC 548

RESULT 11
US-10-920-869-27
; Sequence 27, Application US/10920869
; Publication No. US2005002261A1
; GENERAL INFORMATION:
; APPLICANT: Fincher, Karen
; APPLICANT: Flasinski, Stanislaw
; APPLICANT: Wilkinson, Jack
; TITLE OF INVENTION: Novel Plant Expression Constructs
; FILE REFERENCE: 38-21(51499)B
; CURRENT APPLICATION NUMBER: US/10/920,869
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: US/09/737,626
; PRIOR FILING DATE: 2000-12-15
; PRIOR APPLICATION NUMBER: 09/737,626
; PRIOR FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 27
; LENGTH: 1946
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1946)
; OTHER INFORMATION: chimeric promoter fusion FMV and Act11 polynucleotides +
; OTHER INFORMATION: ntro
US-10-920-869-27
```

US-10-920-869-27

Query Match 19.0%; Score 548; DB 8; Length 1946;
Best Local Similarity 100.0%; Pred. No. 4.5e-96;
Matches 548; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTCAAGGTCAAGGTCAAGGTCTCCAAACATTAGCCAAA 2294
DB 1 AATTCTCAGTCCAAAGCCTCAACAGGTCAAGGTCAAGGTCTCCAAACATTAGCCAAA 60
QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGGACACATGCA 2354
DB 61 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGGACACATGCA 120
QY 2355 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTAAAGTTAGTGGGCATCT 2414
DB 121 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTAAAGTTAGTGGGCATCT 180
QY 2415 TTGAAGTAATCTTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCGAGCAAAAAAGGAAT 2474
DB 181 TTGAAGTAATCTTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCGAGCAAAAAAGGAAT 240
QY 2475 GGTGCGAGAATTGTTAGCGCGACCTACCAAAAGCATCTTTGCCCTTATTTGCAAAAGATAAG 2534
DB 241 GGTGCGAGAATTGTTAGCGCGACCTACCAAAAGCATCTTTGCCCTTATTTGCAAAAGATAAG 300
QY 2535 CAGATTCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAGAGCTGCTCTGACAGCC 2594
DB 301 CAGATTCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAGAGCTGCTCTGACAGCC 360
QY 2595 CACTCACTAATCGGTATGACAAAGCGAGTGAACCAACAAAGAAATTTAGCTTGAAGTCTAG 2654
DB 361 CACTCACTAATCGGTATGACAAAGCGAGTGAACCAACAAAGAAATTTAGCTTGAAGTCTAG 420
QY 2655 GATTAGCAGCATTCAGATTGGTTCAATCAACAGGTACGAGCCATATCATTTATTC 2714
DB 421 GATTAGCAGCATTCAGATTGGTTCAATCAACAGGTACGAGCCATATCATTTATTC 480
QY 2715 AAATTGGTATCGCAAAACCAAGGAATCTCCATCTCAAAAGGTTTGTGAAGGAAGAAT 2774
DB 481 AAATTGGTATCGCAAAACCAAGGAATCTCCATCTCAAAAGGTTTGTGAAGGAAGAAT 540
QY 2775 TCGATATC 2782
DB 541 TCGATATC 548

RESULT 12
US-09-861-696-1
; Sequence 1, Application US/09861696
; Patent No. US2002007053A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS04 MOBT:175-4
; CURRENT APPLICATION NUMBER: US/09/861.696
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1

; LENGTH: 597
; TYPE: DNA
; ORGANISM: Figwort mosaic virus
US-09-861-696-1
Query Match 14.2%; Score 409.2; DB 3; Length 597;
Best Local Similarity 98.1%; Pred. No. 2.5e-69;
Matches 414; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 2235 AATTCTCAGTCCAAAGCCTCAACAGGTCAAGGTCAAGGTCTCCAAACATTAGCCAAA 2294
DB 127 AATTCTCAGTCCAAAGCCTCAACAGGTCAAGGTCAAGGTCTCCAAACATTAGCCAAA 186
QY 2295 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGGACACATGCA 2354
DB 187 AGCTACAGGAGATCAATGAAGAATCTTCAATCAAGTAAACTACTGTTCAGGACACATGCA 246
QY 2355 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTAAAGTTAGTGGGCATCT 2414
DB 247 TCATGGTCACTAAGTTTTCAGAAAAAGACATCCACCGAAGCTTAAAGTTAGTGGGCATCT 306
QY 2415 TTGAAGTAATCTTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCGAGCAAAAAAGGAAT 2474
DB 307 TTGAAGTAATCTTTGTCAACATCGAGCAGCTGGCTTGTGGGGACCGAGCAAAAAAGGAAT 366
QY 2475 GGTGCGAGAATTGTTAGCGCGACCTACCAAAAGCATCTTTGCCCTTATTTGCAAAAGATAAG 2534
DB 367 GGTGCGAGAATTGTTAGCGCGACCTACCAAAAGCATCTTTGCCCTTATTTGCAAAAGATAAG 426
QY 2535 CAGATTCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAGAGCTGCTCTGACAGCC 2594
DB 427 CAGATTCTCTAGTACAAAGTGGGAAACAAATTAACGTGGAAGAGCTGCTCTGACAGCC 486
QY 2595 CACTCACTAATCGGTATGACAAAGCGAGTGAACCAACAAAGAAATTTAGCTTGAAGTCTAG 2654
DB 487 CACTCACTAATCGGTATGACAAAGCGAGTGAACCAACAAAGAAATTTAGCTTGAAGTCTAG 546
QY 2655 GA 2656
DB 547 AA 548

RESULT 13
US-09-464-099A-1
; Sequence 1, Application US/09464099A
; Patent No. US20020168680A1
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard F.
; APPLICANT: Kishore, Ganesh M.
; APPLICANT: Padgett, Stephen R.
; APPLICANT: Stallings, William C.
; TITLE OF INVENTION: GLYPHOSATE TOLERANT 5-ENOLPYRUVYLSHIKIMATE-3-PHOSPHATE SYNTHASES
; FILE REFERENCE: 11899.0175.CNUS01 MOBT:175-2
; CURRENT APPLICATION NUMBER: US/09/464,099A
; CURRENT FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: US 09/137,440
; PRIOR FILING DATE: 1998-08-20
; PRIOR APPLICATION NUMBER: US 08/833,485
; PRIOR FILING DATE: 1997-04-07
; PRIOR APPLICATION NUMBER: US 08/306,063
; PRIOR FILING DATE: 1994-09-13
; PRIOR APPLICATION NUMBER: US 07/749,611
; PRIOR FILING DATE: 1991-08-28
; PRIOR APPLICATION NUMBER: US 07/576,537
; PRIOR FILING DATE: 1990-08-31
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 597
; TYPE: DNA
; ORGANISM: Figwort mosaic virus
US-09-464-099A-1

Qy	2355	TCATGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT	24114
Db	264	TCATGGTCAGTAAAGTTTCAGAAAAAGACATCCACCGAAGACTTTAAAGTTAGTGGGCATCT	323
Qy	2415	TTGAAAGCTAATCTTGTCAAACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAAAAGGAAT	2474
Db	324	TTGAAAGTAAATCTTGTCAAACATCGAGCAGCTGGCTTGTGGGACCCAGACAAAAAAGGAAT	383
Qy	2475	GGTGCAGAAATGTTTAGCGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGATAAAG	2534
Db	384	GGTGCAGAAATGTTTAGCGCGCACCTTACCAAAAGCATCTTTGCCCTTTATTGCAAAAGATAAAG	443
Qy	2535	CAGATTCCTCTAGTACAAAGTGGGAAACAAATAAACGTGGAAGAGCTGCTCGACAGCC	2594
Db	444	CAGATTCCTCTAGTACAAAGTGGGAAACAAATAAACGTGGAAGAGCTGCTCGACAGCC	503
Qy	2595	CACCTCACTAATCGGTATGACGAACCGCAGTCAGACCCACAAAGAAATTAGCTTGAGCTCAG	2654
Db	504	CACCTCACTAATCGGTATGACGAACCGCAGTCAGACCCACAAAGAAATTCCTCTATATAAG	563
Qy	2655	GA 2656	
Db	564	AA 565	

Search completed: March 31, 2006, 07:57:46
Job time : 2214.86 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:01:03 ; Search time 1107.43 Seconds
(without alignments)
10080.402 Million cell updates/sec

Title: US-10-541-346-4

Perfect score: 1675

Sequence: 1 tgaccgaagtaatatgagg.....tagtcgaacctggagaag 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N_Geneseq_21:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002as:*
- 7: Geneseqn2002bs:*
- 8: Geneseqn2003as:*
- 9: Geneseqn2003bs:*
- 10: Geneseqn2003cs:*
- 11: Geneseqn2003ds:*
- 12: Geneseqn2004as:*
- 13: Geneseqn2004bs:*
- 14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1675	100.0	1675	13	ADR46166
2	530.6	31.7	3706	13	ADR49368
3	530.6	31.7	3778	13	ADR49367
4	312.8	18.7	7794	14	AEB71496
5	310	18.5	8012	2	AAx57305
6	310	18.5	8418	2	AAx57309
7	310	18.5	8798	2	AAx57308
8	310	18.5	10846	6	ABs54336
9	310	18.5	10847	2	AAx08923
10	310	18.5	10900	2	AAx08924
11	310	18.5	10900	2	ABs54337
12	310	18.5	11606	12	ADQ13598
13	295	17.6	662	14	ADW69411
14	295	17.6	1998	8	ABV76269
15	289	17.3	12304	8	ABV75876
16	289	17.3	12497	8	ABV75875
17	289	17.3	12614	4	AAC66931
18	282	16.8	632	6	ABN83922
19	280.2	16.7	5365	13	ADU73233

20	280.2	16.7	7713	12	ADQ95182
21	280.2	16.7	7794	14	AEB71496
22	280.2	16.7	8179	12	ADQ95181
23	280.2	16.7	8590	14	AEB71495
24	280.2	16.7	10249	3	AAAL5563
25	280.2	16.7	10312	3	AAAL5564
26	280.2	16.7	10339	3	AAAL5562
c 27	280.2	16.7	10490	6	ABL54627
c 28	280.2	16.7	12739	14	ADW39084
c 29	280.2	16.7	14194	4	AAC66932
c 30	280.2	16.7	15397	2	AAT58635
c 31	280.2	16.7	17511	14	ADV39061
c 32	280.2	16.7	18987	14	ADV39062
c 33	280.2	16.7	24596	1	AAN50182
c 34	280	16.7	1461	14	AEA89731
c 35	280	16.7	7450	14	AEA89733
c 36	278.8	16.6	10603	13	ADU69212
c 37	278.6	16.6	10078	6	ABQ73047
c 38	278.6	16.6	24593	1	AAN50226
c 39	271.4	16.2	10575	13	ADU69210
c 40	271.4	16.2	10677	13	ADU69211
c 41	270.2	16.1	10323	2	AAx90954
c 42	270.2	16.1	15676	3	AAD01288
c 43	270.2	16.1	17111	3	AAD01289
c 44	270.2	16.1	17116	3	AAD01290
45	268.2	16.0	550	13	ADT03989

ALIGNMENTS

RESULT 1

ADR46166

ID ADR46166 standard; DNA; 1675 BP.

XX ADR46166;

XX 18-NOV-2004 (first entry)

DE Glyphosate resistance cotton event MON 88913 3' DNA junction sequence.

XX Glyphosate tolerance; herbicide tolerance; cotton; transgenic; plant;

XX MON 88913; gene; ds.

XX Gossypium hirsutum.

OS Agrobacterium sp.

OS Chimeric.

XX Key Location/Qualifiers

FT misc_difference 600..601

FT /*tag= a

FT /note= "3' junction of transgene and genomic DNA"

XX WO2004072235-A2.

XX 26-AUG-2004.

XX 02-FEB-2004; 2004WO-US002907.

XX 12-FEB-2003; 2003US-0447184P.

XX (MONS) MONSANTO TECHNOLOGY LLC.

XX Cerny RE, Duong C, Hart JL, Huber SA, Krieb RL, Listello JJ;

XX Martens AB, Sammons B;

XX WPI; 2004-625846/60.

XX New seed of cotton event designated MON 88913, useful for producing a

XX cotton plant that tolerates application of glyphosate herbicide to

XX control weeds in crop.

XX Claim 5; SEQ ID NO 4; 50pp; English.

xx The present sequence is the 3' transgene/genomic junction sequence of
cc glyphosate tolerant cotton event MON 88913. This sequence is novel in
cc cotton event MON 88913. A cotton plant and seed comprising the sequence
cc in its genome is an aspect of the invention. Cotton event MON 88913 was
cc generated by an Agrobacterium-mediated transformation of cotton cells
cc with a DNA fragment derived from pMON51915. The DNA fragment contained 2
cc transgene expression cassettes that each included a glyphosate tolerant 5
cc -enol-pyruvylshikimate-3-phosphate synthase (EPSPS) sequence from
cc Agrobacterium sp. strain CP4. The invention is related to the transgenic
cc cotton event MON 88913 having seed deposited at ATCC PTA-4854, and to
cc progeny plants and seeds or their regenerable parts, and cotton plants
cc having a glyphosate tolerant phenotype. Methods are also provided for
cc detecting the presence of DNA corresponding to cotton event MON 88913 in
cc a sample by detecting a transgene/genomic junction region from cotton
cc plant event MON 88913. A DNA primer comprising at least 11 contiguous
cc nucleotides homologous of the present sequence, or its complement, is
cc used in a DNA amplification method to produce an amplicon comprising the
cc 3' junction region ADR46164 diagnostic for cotton event MON 88913. Also
cc provided are methods of producing glyphosate tolerant cotton plants, a
cc method for determining the zygosity of the progeny of cotton event MON
cc 88913, and a method for controlling weeds in a crop or field of cotton
cc event MON 88913 by applying glyphosate herbicide.
xx
SQ Sequence 1675 BP; 633 A; 221 C; 190 G; 631 T; 0 U; 0 Other;

Query Match 100.0%; Score 1675; DB 13; Length 1675;
Best Local Similarity 100.0%; Pred. No. 1.5e-185;
Matches 1675; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGCTAGTGTGACCATTTGCTTATTCACCTA 60
DB 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGCTAGTGTGACCATTTGCTTATTCACCTA 60

QY 61 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGCAATACAAAGTATGTC 120
DB 61 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGCAATACAAAGTATGTC 120

QY 121 CTCTGTGTTTATGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180
DB 121 CTCTGTGTTTATGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180

QY 181 ATTCTAATCATCTCTTTTAAATATATAGTTATCTCATGATTTGTAATGAGTATGAAAA 240
DB 181 ATTCTAATCATCTCTTTTAAATATATAGTTATCTCATGATTTGTAATGAGTATGAAAA 240

QY 241 TATTTTAAATGATTTTATGACTTGCCTGCAATGCAATGCAATGCAATGCAATGCAATGCA 300
DB 241 TATTTTAAATGATTTTATGACTTGCCTGCAATGCAATGCAATGCAATGCAATGCAATGCA 300

QY 301 AGCCACTCGAGTGGAGGCTCATCTAAGCCCCCATTTGGACGTAATGTAGACACGTGCA 360
DB 301 AGCCACTCGAGTGGAGGCTCATCTAAGCCCCCATTTGGACGTAATGTAGACACGTGCA 360

QY 361 AATAAGATTTCCGAATAGAAATTTGTTATGCTTTCGCTTAATATACGCGGAT 420
DB 361 AATAAGATTTCCGAATAGAAATTTGTTATGCTTTCGCTTAATATACGCGGAT 420

QY 421 CGTAATTTGCTGTTTATCAAAATGATCTTTCATTTTAAATAACGCTGCGGACATCTAC 480
DB 421 CGTAATTTGCTGTTTATCAAAATGATCTTTCATTTTAAATAACGCTGCGGACATCTAC 480

QY 481 ATTTTGAATGAAAAAATTTGGTAATTAATCTCTTTTTCCTATATGACCAATCAT 540
DB 481 ATTTTGAATGAAAAAATTTGGTAATTAATCTCTTTTTCCTATATGACCAATCAT 540

QY 541 ACTCATTTGCTGATCCATGAGATTTCCGACGATGAAGCCATTTTAAATGATATAT 600
DB 541 ACTCATTTGCTGATCCATGAGATTTCCGACGATGAAGCCATTTTAAATGATATAT 600

QY 601 TACAAAGCTATTTGCTTATTAACATATGCGAAAAATTTTGTACTATTAATCAGGGGTAAAT 660
DB 601 TACAAAGCTATTTGCTTATTAACATATGCGAAAAATTTTGTACTATTAATCAGGGGTAAAT 660

RESULT 2
ADR49368
ID ADR49368 standard; DNA; 3706 BP.

QY 661 TAGGAGGGGCTGTAGTCTCGCTTCTTAAATGAAAAATTTTCTATTTAGTTATTT 720
DB 661 TAGGAGGGGCTGTAGTCTCGCTTCTTAAATGAAAAATTTTCTATTTAGTTATTT 720

QY 721 AAAATTTTAAAAAGTAAAAATATAAAAATTTTCATTTAATCCTTTAAAAAATATAAGATATA 780
DB 721 AAAATTTTAAAAAGTAAAAATATAAAAATTTTCATTTAATCCTTTAAAAAATATAAGATATA 780

QY 781 GACTATTTAAATGATGAATTAACAATTTTATATCATAAAAATATAAATTTAATTTTCGAC 840
DB 781 GACTATTTAAATGATGAATTAACAATTTTATATCATAAAAATATAAATTTAATTTTCGAC 840

QY 841 CCTTAACAAAAATTTTCTGATTTTGGCCCTAAGCTGTAATTTTGTATAAAAACATTTTCTT 900
DB 841 CCTTAACAAAAATTTTCTGATTTTGGCCCTAAGCTGTAATTTTGTATAAAAACATTTTCTT 900

QY 901 TTTGCAATTTAATGATTTCTTTAATTCAGTCCCAAGAAAGAAATTTTATAATTCGATATGCG 960
DB 901 TTTGCAATTTAATGATTTCTTTAATTCAGTCCCAAGAAAGAAATTTTATAATTCGATATGCG 960

QY 961 AAAGTTAGTCTTGGCTAGTGATATTAAGGAAAGAAACATAAAAATCAATAATTAATTT 1020
DB 961 AAAGTTAGTCTTGGCTAGTGATATTAAGGAAAGAAACATAAAAATCAATAATTAATTT 1020

QY 1021 TTAAGCAAAATAGTAAAAATTAAGGAAAGAAATTTTCTACGATAGTCTATAATTTCAAAAAAAG 1080
DB 1021 TTAAGCAAAATAGTAAAAATTAAGGAAAGAAATTTTCTACGATAGTCTATAATTTCAAAAAAAG 1080

QY 1081 AAATAATTAATCTTTAAACCAATGAAATTTTAAAAATTAACATCAGAAATTAATCTATTTAAT 1140
DB 1081 AAATAATTAATCTTTAAACCAATGAAATTTTAAAAATTAACATCAGAAATTAATCTATTTAAT 1140

QY 1141 TTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1200
DB 1141 TTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1200

QY 1201 AATCAATAAATAAATTTCTTACAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260
DB 1201 AATCAATAAATAAATTTCTTACAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1260

QY 1261 ATATATTTTATACAGACATATAGAAATATAAATAAATAAATAAATAAATAAATAAATAA 1320
DB 1261 ATATATTTTATACAGACATATAGAAATATAAATAAATAAATAAATAAATAAATAAATAA 1320

QY 1321 TTTAATTTTAAACATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1380
DB 1321 TTTAATTTTAAACATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1380

QY 1381 AATTTTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1440
DB 1381 AATTTTATATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1440

QY 1441 AATCTACTTTTAAATTAAGTCTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1500
DB 1441 AATCTACTTTTAAATTAAGTCTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1500

QY 1501 ATCTGATAATATCTTAACCCCTTTTATAAATAAATAAATAAATAAATAAATAAATAAATAA 1560
DB 1501 ATCTGATAATATCTTAACCCCTTTTATAAATAAATAAATAAATAAATAAATAAATAAATAA 1560

QY 1561 AATATCATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1620
DB 1561 AATATCATTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1620

QY 1621 GGTAGTAAAACTCATTACACATTTTAAAGTAGAACGTAGTTTCGAACCTTGGAGAG 1675
DB 1621 GGTAGTAAAACTCATTACACATTTTAAAGTAGAACGTAGTTTCGAACCTTGGAGAG 1675

XX ADR49368;
 XX 18-NOV-2004 (first entry)
 XX H7-1 transformant-associated DNA fragment #1.
 XX
 KW ds; plant; glyphosate-resistance; sugar beet; seed;
 KW glyphosate-tolerant sugar beet; chloroplast transit peptide;
 KW 5-enolpyruvyl-shikimate-3-phosphate synthase; EPSPS; H7-1 transformant;
 KW T-DNA; CP4-EPSPS.
 XX Unidentified.
 OS
 XX WO2004074492-A1.
 XX
 XX 02-SEP-2004.
 XX 17-FEB-2004; 2004WO-EP001469.
 XX
 XX 20-FEB-2003; 2003EP-00003866.
 PR 28-FEB-2003; 2003US-00376763.
 XX
 PA (KWSS-) KWS SAAT AG.
 XX
 PI Kraus J, Sauerbrey E, Nehls R, Looock A, Jansen R;
 XX WPI; 2004-652964/63.
 XX
 XX New sugar beet plants resistant to glyphosate, contain inserted 5-
 PT enolpyruvyl-shikimate-3-phosphate synthase gene, which is stably
 PT integrated and inherited.
 XX
 PS Claim 2; SEQ ID NO 6; 79pp; German.
 XX
 CC This invention describes novel glyphosate-resistant Glycine max (sugar
 CC beet) plants derived from seeds deposited as NCIMB 41158 or 41159. The
 CC invention also describes a method for identifying glyphosate-tolerant
 CC sugar beet and a test kit for identifying glyphosate-tolerant sugar beet,
 CC or their cells, tissues and parts. The novel kit comprises at least one
 CC primer pair, where one primer recognizes a foreign DNA inserted into the
 CC genome, while the second recognises DNA within a flanking (3' or 5')
 CC region. The plants are prepared by Agrobacterium-mediated transformation
 CC of sugar beet, using the vector pV-BVGT08, which contains, between right
 CC and left border sequences, a cassette containing the coding regions for
 CC (a) chloroplast transit peptide and (b) the enzyme 5-enolpyruvyl-
 CC shikimate-3-phosphate synthase (EPSPS) from Arabidopsis thaliana, under
 CC control of the figwort mosaic virus promoter and the E9-3'
 CC transcriptional terminator of Pisum sativum. One transformation event (H7
 CC -1), which produced plants of high tolerance to glyphosate, was
 CC characterised and found to contain an insertion of a single, intact copy
 CC of the T-DNA, including the regulatory components, from pV-BVGT08. The
 CC genomic sequences outside the insert region were identical with those in
 CC a non-transformed plant and the insert was integrated stably and inherited
 CC stably. The novel plants are highly resistant to glyphosate and retain
 CC good properties as regards growth, yield, quality and resistance to
 CC pathogens. This sequence represents a fragment of the H7-1 transformant
 CC DNA found in vector pV-BVGT08.
 XX
 SQ Sequence 3706 BP; 943 A; 801 C; 801 G; 1161 T; 0 U; 0 Other;
 Query Match 31.7%; Score 530.6; DB 13; Length 3706;
 Best Local Similarity 92.9%; Pred. No. 2.8e-53;
 Matches 592; Conservative 0; Mismatches 9; Indels 36; Gaps 2;
 XX
 QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTATGCTTATTCTACTA 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3032 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTATGCTTATTCTACTA 3091
 QY 61 GGCAACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3092 GGCAACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 3151

QY 121 CTCCTGTGTTTAGACATTTATGAACCTTCCTTTATGTAAATTTTCCAGAAATCCTTGTGAG 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3152 CTCCTGTGTTTAGACATTTATGAACCTTCCTTTATGTAAATTTTCCAGAAATCCTTGTGAG 3211
 QY 181 ATTCTAATCATTTGCTTTTATAAATTATATATCTATCTATGATGTTGTAGTATGAAAA 240
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3212 ATTCTAATCATTTGCTTTTATAAATTATATATCTATCTATGATGTTGTAGTATGAAAA 3271
 QY 241 TATTTTTTAATGCATTTTATGCTTCCCAATTCATTGACAAACATGTCATCAATCGACTGC 300
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3272 TATTTTTTAATGCATTTTATGCTTCCCAATTCATTGACAAACATGTCATCAATCGACTGC 3331
 QY 301 AGCCACTCGAGTGG-----AGGCTCATCT 325
 DB |||||||||||
 DB 3332 AGCCACTCGAGCGCGCCACTCGAGTGGTGGCCCGCATGCTGTAAGTTTCTCATCT 3391
 QY 326 AAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 385
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3392 AAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 3451
 QY 386 TTGTTTTATGCTTTTCGCTTATAAATACGACGATCGTAATTTGTCTGTTTATCAAAATG 445
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3452 TTGTTTTATGCTTTTCGCTTATAAATACGACGATCGTAATTTGTCTGTTTATCAAAATG 3511
 QY 446 TACTTTTCATTTTATAATAACGTCGCGACATCTACATTTTGAATTTGAAAAAATTTGGT 505
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3512 TACTTTTCATTTTATAATAACGTCGCGACATCTACATTTTGAATTTGAAAAAATTTGGT 3570
 QY 506 AATTACTCTTTCTTTTCTCCATATTGACCATCATCTATCTGCTGATCCATGATGATTTT 565
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3571 AATTACTCTTTCTTTTCTCCATATTGACCATCATCTATCTGCTGATCCATGATGATTTT 3630
 QY 566 CCGGACATGAGCCATTTCACAAATTCGAATATATATTA 602
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 3631 CCGGACATGAGCCATTTCACAAATTCGAATATATATTA 3667
 RESULT 3
 ADR49367
 ID ADR49367 standard; DNA; 3778 BP.
 XX
 AC ADR49367;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Vector pV-BVGT08 H7-1 transformant insert.
 XX
 KW ds; plant; glyphosate-resistance; sugar beet; seed;
 KW glyphosate-tolerant sugar beet; chloroplast transit peptide;
 KW 5-enolpyruvyl-shikimate-3-phosphate synthase; EPSPS; H7-1 transformant;
 KW T-DNA; pV-BVGT08.
 XX
 OS Synthetic.
 XX
 PN WO2004074492-A1.
 XX
 PD 02-SEP-2004.
 XX
 PF 17-FEB-2004; 2004WO-BP001469.
 XX
 PR 20-FEB-2003; 2003EP-00003866.
 PR 28-FEB-2003; 2003US-00376763.
 XX
 PA (KWSS-) KWS SAAT AG.
 XX
 PI Kraus J, Sauerbrey E, Nehls R, Looock A, Jansen R;
 XX WPI; 2004-652964/63.
 XX
 XX New sugar beet plants resistant to glyphosate, contain inserted 5-
 PT enolpyruvyl-shikimate-3-phosphate synthase gene, which is stably
 PT integrated and inherited.
 XX

PS Claim 14; SEQ ID NO 5; 79pp; German.

CC This invention describes novel glyphosate-resistant Glycine max (sugar
CC beet) plants derived from seeds deposited as NCIMB 41158 or 41159. The
CC invention also describes a method for identifying glyphosate-tolerant
CC sugar beet and a test kit for identifying glyphosate-tolerant sugar beet,
CC or their cells, tissues and parts. The novel kit comprises at least one
CC primer pair, where one primer recognizes a foreign DNA inserted into the
CC genome, while the second recognises DNA within a flanking (3' or 5')
CC region. The plants are prepared by Agrobacterium-mediated transformation
CC of sugar beet, using the vector pV-BVGT08, which contains, between right
CC and left border sequences, a cassette containing the coding regions for
CC (a) chloroplast transit peptide and (b) the enzyme 5-enolpyruvyl-
CC shikimate-3-phosphate synthase (EPSPS) from Arabidopsis thaliana, under
CC control of the figwort mosaic virus promoter and the E9-3'
CC transcriptional terminator of Pisum sativum. One transformation event (H7
CC -1), which produced plants of high tolerance to glyphosate, was
CC characterised and found to contain an insertion of a single, intact copy
CC of the T-DNA, including the regulatory components, from pV-BVGT08. The
CC genomic sequences outside the insert region were identical with those in
CC a non-transformed plant and the insert was integrate stably and inherited
CC stably. The novel plants are highly resistant to glyphosate and retain
CC good properties as regards growth, yield, quality and resistance to
CC pathogens. This sequence represents the vector pV-GVGT08 H7-1
CC transformant insert.

XX Sequence 3778 BP; 958 A; 822 C; 823 G; 1175 T; 0 U; 0 Other;

Query Match 31.7%; Score 530.6; DB 13; Length 3778;

Best Local Similarity 92.9%; Pred. No. 2.8e-53;

Matches 592; Conservative 0; Mismatches 9; Indels 36; Gaps 2;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTTAGTTGTATACCATTTATTCACATA 60
DB 3077 TGACCGAAGTTAATATGAGGAGTAAACACTTGTTAGTTGTATACCATTTATTCACATA 3136
QY 61 GGCACAAATATATTTTCAGACTAGAAAGCTGCAAAAGTTACTGAAATACAAAGTATGTC 120
DB 3137 GGCACAAATATATTTTCAGACTAGAAAGCTGCAAAAGTTACTGAAATACAAAGTATGTC 3196
QY 121 CTCCTGTGTTTAGACATTTATGAATTTCTTTTATGTAAATTTCCAGAAATCCTTGTCAG 180
DB 3197 CTCCTGTGTTTAGACATTTATGAATTTCTTTTATGTAAATTTCCAGAAATCCTTGTCAG 3256
QY 181 ATCTAATCATGCTTTTAAATATATAGTTATATCTATGGAATTTAGTTGAGTATGAAA 240
DB 3257 ATCTAATCATGCTTTTAAATATATAGTTATATCTATGGAATTTAGTTGAGTATGAAA 3316
QY 241 TATTTTAAATCATTTTATGACTTGCCAAATGATTGACAAATGATGCAATCAATCGACCTGC 300
DB 3317 TATTTTAAATCATTTTATGACTTGCCAAATGATTGACAAATGATGCAATCAATCGACCTGC 3376
QY 301 AGCCACTCGAGTGG-----AGCCCTCATCT 325
DB 3377 AGCCACTCGAGCGCGCCACTCGAGTGGTGGCCGATCGATCGTGAAGTTTCTCATCT 3436
QY 326 AAGCCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATA 385
DB 3437 AAGCCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTAGAATA 3496
QY 386 TTTGTTTATGCTTTTCGCTATATAATACGACGATGTAATTTGCTGTTTATCAAAATG 445
DB 3497 TTTGTTTATGCTTTTCGCTATATAATACGACGATGTAATTTGCTGTTTATCAAAATG 3556
QY 446 TACTTTTCAATTAATACGCTGGGACATCTACATTTTTCGAATTTGAAAAAATTTGTT 505
DB 3557 TACTTTTCAATTAATACGCTGGGACATCTACATTTTTCGAATTTGAAAAAATTTGTT 3615
QY 506 AATTAATCTTTCTTTTCCATATAGGACATCATCTACTCATCTGCTGATCCATGATGATTT 565
DB 3616 AATTAATCTTTCTTTTCCATATAGGACATCATCTACTCATCTGCTGATCCATGATGATTT 3675
QY 566 CCCGGACATGAAGCCATTTTACAATTTGAATATATATTA 602

DB 3676 CCCGACATGAGCCATTACAAATGGAATATATCCTA 3712

RESULT 4

ABE71496/c

ID AEB71496 standard; DNA; 7794 BP.

XX AEB71496;

AC AEB71496;

XX 20-OCT-2005 (first entry)

DT A. tumefaciens transformation vector DNA SEQ ID NO:2.

DE A. tumefaciens transformation vector DNA; transgenic plant; ds.

XX vector; recombinant DNA; transgenic plant; ds.

XX Agrobacterium tumefaciens.

OS Pisum sativum.

OS Zea mays.

XX Key Location/Qualifiers

FT misc_feature 1..357

FT /tag= a

FT /note= "A. tumefaciens right border"

FT misc_feature 376..1774

FT /tag= b

FT /note= "Rice actin promoter and intron"

FT CDS 1784..2011

FT /tag= c

FT /product= "A. tumefaciens EPSPS chloroplast transit

FT peptide"

FT CDS 2012..3379

FT /tag= d

FT /product= "A. tumefaciens aroA"

FT misc_feature 3395..3647

FT /tag= e

FT /note= "A. tumefaciens NOS terminator"

FT misc_feature 3479..4391

FT /tag= f

FT /note= "Pisum sativum RbcS2 terminator"

FT misc_feature 4398..4748

FT /tag= g

FT /note= "Zea mays alpha zein gene Z19s fragment"

FT misc_feature 4755..5043

FT /tag= h

FT /note= "Zea mays alpha zein gene Z22s fragment"

FT misc_feature 5050..5835

FT /tag= i

FT /note= "Zea mays alpha zein gene Z22asL fragment"

FT misc_feature 5842..6192

FT /tag= j

FT /note= "Zea mays alpha zein gene Z19as fragment"

FT misc_feature 6204..7305

FT /tag= k

FT /note= "Zea mays gamma zein gene Z27 promoter"

FT misc_feature 7353..7794

FT /tag= l

FT /note= "A. tumefaciens left border"

XX US2005176670-A1.

XX 11-AUG-2005.

XX 10-FEB-2005; 2005US-00057062.

XX 10-FEB-2004; 2004US-0543157P.

XX 10-FEB-2004; 2004US-0543187P.

XX 11-AUG-2004; 2004US-0600859P.

XX (HUAN/) HUANG S.

XX (MALV/) MALVAR T M.

XX (LUET/) LUETHY M H.

DT 20-MAR-2003 (revised)
XX 26-JUL-1999 (first entry)
XX
DE Sugar beet T-DNA containing cp4/epsps #2.
XX
XX Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
XX
XX Beta vulgaris.
OS
XX
XX WO9923232-A1.
XX
XX 14-MAY-1999.
XX
XX 29-OCT-1998; 98WO-EP006859.
XX
XX 31-OCT-1997; 97US-00962467.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Mannerloef M, Tenning PP, Steen P;
PI
XX
XX WPI; 1999-313347/26.
XX
XX Glyphosate resistant transgenic sugar beet plants.
XX
XX Claim 15; Page 36-41; 55pp; English.
XX
XX This invention describes a novel sugar beet plant, including its
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated
CC transformation with a gene allowing expression of cp4/epsps in plants,
CC where the plant lacks both right and left T-DNA border sequences. The
CC transgenic sugar beet plants of the invention are capable of tolerating
CC herbicide treatment with glyphosate (also known as N-phosphonomethyl-
CC glycine) as the active ingredient, e.g. Roundup. (Updated on 20-MAR-2003
CC to correct PR field.)
XX
XX Sequence 8418 BP; 2170 A; 1976 C; 1976 G; 2296 T; 0 U; 0 Other;
SQ
Query Match 18.5%; Score 310; DB 2; Length 8418;
Best Local Similarity 100.0%; Pred. No. 7.7e-28;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTATGCTTATTCACCTA 60
Db 2687 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTATGCTTATTCACCTA 2746
QY 61 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAATGTTACTGCAATACAAGTATGTC 120
Db 2747 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAATGTTACTGCAATACAAGTATGTC 2806
QY 121 CTCCTGTGTTTTAGACATTTATGCACTTTCCTTTATGTAATTTTCCAGAAATCCTTCTCAG 180
Db 2807 CTCCTGTGTTTTAGACATTTATGCACTTTCCTTTATGTAATTTTCCAGAAATCCTTCTCAG 2866
QY 181 ATTCCTAATCATGCTTTTATAATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 240
Db 2867 ATTCCTAATCATGCTTTTATAATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 2926
QY 241 TATTTTTTAATGCAATTTATGACTTGCCTGCAATTTGATTTGACAAATGCAATCATGCACTGCG 300
Db 2927 TATTTTTTAATGCAATTTATGACTTGCCTGCAATTTGATTTGACAAATGCAATCATGCACTGCG 2986
QY 301 AGCCACTCGA 310
Db 2987 AGCCACTCGA 2996

RESULT 7
AA57308

ID AAX57308 standard; DNA; 8798 BP.
XX
AC AAX57308;
XX
XX 20-MAR-2003 (revised)
DT 26-JUL-1999 (first entry)
XX
XX Sugar beet T-DNA containing cp4/epsps.
XX
XX Sugar beet; transformation; T-DNA; insertion; cp4/epsps; plant;
KW 5-enolpyruvylshikimate-3-phosphate synthase; transgenic; herbicide;
KW tolerant; glyphosate; Roundup; N-phosphonomethyl-glycine; ss.
XX
XX Beta vulgaris.
OS
XX
XX WO9923232-A1.
XX
XX 14-MAY-1999.
XX
XX 29-OCT-1998; 98WO-EP006859.
XX
XX 31-OCT-1997; 97US-00962467.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
XX Mannerloef M, Tenning PP, Steen P;
PI
XX
XX WPI; 1999-313347/26.
XX
XX Glyphosate resistant transgenic sugar beet plants.
XX
XX Claim 11; Page 31-36; 55pp; English.
XX
XX This invention describes a novel sugar beet plant, including its
CC descendants expressing 5-enolpyruvylshikimate-3-phosphate synthase
CC (cp4/epsps) enzyme activity which is obtainable by Agrobacterium mediated
CC transformation with a gene allowing expression of cp4/epsps in plants,
CC where the plant lacks both right and left T-DNA border sequences. The
CC transgenic sugar beet plants of the invention are capable of tolerating
CC herbicide treatment with glyphosate (also known as N-phosphonomethyl-
CC glycine) as the active ingredient, e.g. Roundup. (Updated on 20-MAR-2003
CC to correct PR field.)
XX
XX Sequence 8798 BP; 2346 A; 1999 C; 2032 G; 2421 T; 0 U; 0 Other;
SQ
Query Match 18.5%; Score 310; DB 2; Length 8798;
Best Local Similarity 100.0%; Pred. No. 7.7e-28;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTATGCTTATTCACCTA 60
Db 2797 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTATGCTTATTCACCTA 2856
QY 61 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAATGTTACTGCAATACAAGTATGTC 120
Db 2857 GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAATGTTACTGCAATACAAGTATGTC 2916
QY 121 CTCCTGTGTTTTAGACATTTATGCACTTTCCTTTATGTAATTTTCCAGAAATCCTTCTCAG 180
Db 2917 CTCCTGTGTTTTAGACATTTATGCACTTTCCTTTATGTAATTTTCCAGAAATCCTTCTCAG 2976
QY 181 ATTCCTAATCATGCTTTTATAATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 240
Db 2977 ATTCCTAATCATGCTTTTATAATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAA 3036
QY 241 TATTTTTTAATGCAATTTATGACTTGCCTGCAATTTGATTTGACAAATGCAATCATGCACTGCG 300
Db 3037 TATTTTTTAATGCAATTTATGACTTGCCTGCAATTTGATTTGACAAATGCAATCATGCACTGCG 3096
QY 301 AGCCACTCGA 310
Db 3097 AGCCACTCGA 3106

RESULT 8
 ID ABS54336 standard; DNA; 10846 BP.
 XX
 AC ABS54336;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE E. coli fda gene, plant transformation vector pMON17524.
 XX
 KW Fructose-1,6-bisphosphate aldolase; FDA; triosephosphate;
 KW plant chloroplast; starch synthesis; cytosol; sucrose synthesis;
 KW carbon assimilation; carbon storage; carbon export; transgenic; potato;
 KW food production; French fry; photosynthesis; plant yield; plant growth;
 KW potato tuber; blanch; dry; par-fry; cyclic; circular; ds.
 XX
 OS Escherichia coli.
 OS Arabidopsis sp.
 OS Figwort mosaic virus.
 OS Synthetic.
 XX
 PN US6441277-B1.
 XX
 PD 27-AUG-2002.
 XX
 PF 16-JUN-1998; 98US-00098219.
 XX
 PR 17-JUN-1997; 97US-0049955P.
 XX
 PA (MONS) MONSANTO TECHNOLOGY LLC.
 XX
 PI Barry GF, Cheikh N, Kishore GM;
 XX
 DR WPI; 2002-711539/77.
 XX
 PT Novel recombinant, DNA molecule for producing genetically transformed
 PT plants having elevated carbon assimilation, has promoter functional in
 PT plant cells, and DNA sequence encoding fructose-1,6-bisphosphate
 PT aldolase.
 XX
 PS Example 2; Col 35-44; 39pp; English.
 XX
 CC The present invention relates to a recombinant, double-stranded DNA
 CC vector, comprising a promoter functional in plant cells, and a DNA
 CC sequence from a prokaryotic organism (e.g. Escherichia coli) coding for
 CC fructose-1,6-bisphosphate aldolase (FDA), where the DNA sequence is
 CC operatively linked to the promoter in the sense orientation. FDA
 CC catalyses the conversion of triosephosphate into fructose-1,6
 CC bisphosphate in plant chloroplasts (starch synthesis) and in the cytosol
 CC (sucrose synthesis). The recombinant DNA vector of the invention is
 CC useful for producing genetically transformed plants that have elevated
 CC carbon assimilation, storage, export and improved uniformity of solids
 CC (e.g. in transgenic potatoes expressing fda). The vector of the invention
 CC is particularly useful in the commercial production of foods derived from
 CC potatoes which are useful for producing French fries. The transgenic
 CC plants exhibit increased photosynthesis rate, increased plant yield,
 CC increased growth rate and increased solids uniformity compared with
 CC plants that do not contain the recombinant DNA vector. The recombinant
 CC DNA vector provides higher quality, more uniform potato tuber regions,
 CC and therefore french fries. This results in a higher throughput in the
 CC French fry processing plant due to lower processing times, and processor
 CC cost savings due to lower energy input required for lower blanch, dry,
 CC and par-fry times. The present sequence represents a plant transformation
 CC vector containing the E. coli fda gene
 XX
 SQ Sequence 10846 BP; 2669 A; 2760 C; 2681 G; 2736 T; 0 U; 0 Other;
 Query Match 18.5%; Score 310; DB 6; Length 10846;
 Best Local Similarity 100.0%; Pred. No. 7.4e-28;
 Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGTACCATTTATGCTTATCTACTA 60
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 2059 TGACCGAAGTTAATATGAGGAGTAAACACTTGTAGTTGTACCATTTATGCTTATCTACTA 2118
 QY 61 GGCAACAATATATTTTTCAGACCTAGAAAGCTGCAAAAGCTTTACTGAAATCAAGTATGTC 120
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 2119 GGCAACAATATATTTTTCAGACCTAGAAAGCTGCAAAAGCTTTACTGAAATCAAGTATGTC 2178
 QY 121 CTCTTGTTGTTTAGACATTTTATGAACCTTTCCTTTATGTATTTTCCAGAAATCCTTGTGTCAG 180
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 2179 CTCTTGTTGTTTAGACATTTTATGAACCTTTCCTTTATGTATTTTCCAGAAATCCTTGTGTCAG 2238
 QY 181 ATTCTAATCATCTGCTTTTATTAATTTATAGTTATATCTATGATTTGTAGTGATGAGTATGAAAA 240
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 2239 ATTCTAATCATCTGCTTTTATTAATTTATAGTTATATCTATGATTTGTAGTGATGAGTATGAAAA 2298
 QY 241 TATTTTAAATGATTTTATGACTTCCCAATTCATTCGACCAATGCAATCATCATGACCTGC 300
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 2299 TATTTTAAATGATTTTATGACTTCCCAATTCATTCGACCAATGCAATCATCATGACCTGC 300
 QY 301 AGCCACTCGA 310
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 2359 AGCCACTCGA 2368
 XX
 RESULT 9
 AAX08923
 ID AAX08923 standard; DNA; 10847 BP.
 XX
 AC AAX08923;
 XX
 DT 27-APR-1999 (first entry)
 XX
 DE Vector comprising fructose-1,6-bisphosphate aldolase (FDA) gene.
 XX
 KW Fructose-1,6-bisphosphate aldolase; FDA; carbon assimilation; starch;
 KW sucrose; crop; yield; growth; transgenic plant; potato; photosynthesis;
 KW ds.
 XX
 OS Synthetic.
 OS
 PN WO9858069-A1.
 XX
 PD 23-DEC-1998.
 XX
 PF 16-JUN-1998; 98WO-US012447.
 XX
 PR 17-JUN-1997; 97US-0049955P.
 XX
 PA (MONS) MONSANTO CO.
 XX
 PI Barry GF, Cheikh N, Kishore GM;
 XX
 DR WPI; 1999-095343/08.
 XX
 PT Use of fructose-1,6-triphosphate aldolase DNA - useful for, e.g.
 PT producing transgenic plants with increased photosynthesis rates,
 PT increased yields, increased growth rates and improved solids uniformity.
 XX
 PS Example 2; Page 51-54; 75pp; English.
 XX
 CC Fructose-1,6-bisphosphate aldolase (FDA) catalyses the reversible
 CC reaction converting triosephosphate into fructose-1,6-bisphosphate
 CC aldolase. By inserting the FDA gene into expression vectors and inserting
 CC these vectors into the chloroplasts of plant cells, increased starch
 CC production can be achieved. Increasing the expression of the FDA enzyme
 CC in the chloroplast increases carbon assimilation and results in an
 CC increase in chloroplast starch production. This increase in carbon
 CC assimilation is a desirable trait in crop plants and leads to increased
 CC plant growth, storage ability, yield, vigour, and stress tolerance.
 CC Increasing FDA expression in the cytosol of photosynthetic cells leads to
 CC an increase in sucrose production. The transgenic plants containing the
 CC recombinant DNA can have increased photosynthesis rates, increased

```
CC yields, increased growth rates and improved solids uniformity compared
CC with plants that do not contain the recombinant DNA molecule. Vectors
CC containing the recombinant FDA gene are used particularly for improving
CC potato products. This sequence describes the vector designated pMON17524
CC which comprises the E.coli FDA gene fused to the Arabidopsis small
CC subunit CTP1. This vector was used for tobacco plant transformation
XX
SQ Sequence 10847 BP; 2669 A; 2760 C; 2681 G; 2736 T; 0 U; 1 Other;

Query Match      18.5%; Score 310; DB 2; Length 10847;
Best Local Similarity 100.0%; Pred. No. 7.4e-28;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGACCATTTATGCTTATTCACCTA 60
DB 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGACCATTTATGCTTATTCACCTA 2118

QY 61 GGCACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAAATCAAGATATGTC 120
DB 2119 GGCACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAAATCAAGATATGTC 2178

QY 121 CTCTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180
DB 2179 CTCTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 2238

QY 181 ATTCTAATCATTCGCTTTTATATATATAGTTACTCATGGATTTGTAGTTGAGTATGAAA 240
DB 2239 ATTCTAATCATTCGCTTTTATATATATAGTTACTCATGGATTTGTAGTTGAGTATGAAA 2298

QY 241 TATTTTTTAAATGCAATTTTATGACTTGGCAATTGATTGACAAATGCAATCAATCGACTGC 300
DB 2299 TATTTTTTAAATGCAATTTTATGACTTGGCAATTGATTGACAAATGCAATCAATCGACTGC 2358

QY 301 AGCCACTCGA 310
DB 2359 AGCCACTCGA 2368

RESULT 10
AA08924
ID AA08924 standard; DNA; 10900 BP.
XX
AC AA08924;
XX
DT 27-APR-1999 (first entry)
XX
XX Vector comprising fructose-1,6-bisphosphate aldolase (FDA) gene.
XX
XX Fructose-1,6-bisphosphate aldolase; FDA; carbon assimilation; starch;
KW sucrose; crop; yield; growth; transgenic plant; potato; photosynthesis;
KW
KW db.
XX
OS Synthetic.
XX
XX WO9858069-A1.
XX
XX 23-DEC-1998.
XX
XX 16-JUN-1998; 98WO-US012447.
XX
XX 17-JUN-1997; 97US-0049955P.
XX
XX (MONS ) MONSANTO CO.
XX
XX Barry GF, Cheikh N, Kishore GM;
XX
XX WPI; 1999-095343/08.
XX
XX Use of fructose-1,6-triphosphate aldolase DNA - useful for, e.g.
PT producing transgenic plants with increased photosynthesis rates,
PT increased yields, increased growth rates and improved solids uniformity.
XX
XX Example 2; Page 55-58; 75pp; English.
XX
```

```
XX Fructose-1,6-bisphosphate aldolase (FDA) catalyses the reversible
CC reaction converting triosephosphate into fructose-1,6-bisphosphate
CC aldolase. By inserting the FDA gene into expression vectors and inserting
CC these vectors into the chloroplasts of plant cells, increased starch
CC production can be achieved. Increasing the expression of the FDA enzyme
CC in the chloroplast increases carbon assimilation and results in an
CC increase in chloroplast starch production. This increase in carbon
CC assimilation is a desirable trait in crop plants and leads to increased
CC plant growth, storage ability, yield, vigour, and stress tolerance.
CC Increasing FDA expression in the cytosol of photosynthetic cells leads to
CC an increase in sucrose production. The transgenic plants containing the
CC recombinant DNA can have increased photosynthesis rates, increased
CC yields, increased growth rates and improved solids uniformity compared
CC with plants that do not contain the recombinant DNA molecule. Vectors
CC containing the recombinant FDA gene are used particularly for improving
CC potato products. This sequence describes the vector designated pMON17542
CC which comprises the E.coli FDA gene fused to the Arabidopsis small
CC subunit CTP1 and the Arabidopsis EPSPS (CTP2) transit peptide. This
CC vector was used for tobacco plant transformation
XX
SQ Sequence 10900 BP; 2691 A; 2750 C; 2694 G; 2764 T; 0 U; 1 Other;

Query Match      18.5%; Score 310; DB 2; Length 10900;
Best Local Similarity 100.0%; Pred. No. 7.4e-28;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGACCATTTATGCTTATTCACCTA 60
DB 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGACCATTTATGCTTATTCACCTA 2118

QY 61 GGCACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAAATCAAGATATGTC 120
DB 2119 GGCACAAATATATTTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAAATCAAGATATGTC 2178

QY 121 CTCTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 180
DB 2179 CTCTGTGTTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTCTAG 2238

QY 181 ATTCTAATCATTCGCTTTTATATATATAGTTACTCATGGATTTGTAGTTGAGTATGAAA 240
DB 2239 ATTCTAATCATTCGCTTTTATATATATAGTTACTCATGGATTTGTAGTTGAGTATGAAA 2298

QY 241 TATTTTTTAAATGCAATTTTATGACTTGGCAATTGATTGACAAATGCAATCAATCGACTGC 300
DB 2299 TATTTTTTAAATGCAATTTTATGACTTGGCAATTGATTGACAAATGCAATCAATCGACTGC 2358

QY 301 AGCCACTCGA 310
DB 2359 AGCCACTCGA 2368

RESULT 11
ABS54337
ID ABS54337 standard; DNA; 10900 BP.
XX
AC ABS54337;
XX
XX 12-DEC-2002 (first entry)
XX
XX E. coli fda gene, plant transformation vector pMON17542.
XX
XX Fructose-1,6-bisphosphate aldolase; FDA; triosephosphate;
KW plant chloroplast; starch synthesis; cytosol; sucrose synthesis;
KW carbon assimilation; carbon storage; carbon export; transgenic; potato;
KW food production; French fry; photosynthesis; plant yield; plant growth;
KW potato tuber; blanch; dry; par-fry; cyclic; circular; da.
XX
XX Escherichia coli.
OS Arabidopsis sp.
OS Figwort mosaic virus.
OS Synthetic.
XX
```

PN US6441277-B1.
XX
PD 27-AUG-2002.
XX
PF 16-JUN-1998; 98US-00098219.
XX
PR 17-JUN-1997; 97US-0049995P.
XX
PA (MONS) MONSANTO TECHNOLOGY LLC.
XX
PI Barry GF, Cheikh N, Kishore GM;
XX
XX WPI; 2002-711539/77.
DR
XX Novel recombinant, DNA molecule for producing genetically transformed
XX plants having elevated carbon assimilation, has promoter functional in
XX plant cells, and DNA sequence encoding fructose-1,6-bisphosphate
XX aldolase.
XX
PS Example 2; Col 45-54; 39pp; English.
XX
CC The present invention relates to a recombinant, double-stranded DNA
CC vector, comprising a promoter functional in plant cells, and a DNA
CC sequence from a prokaryotic organism (e.g. *Escherichia coli*) coding for
CC fructose-1,6-bisphosphate aldolase (fda), where the DNA sequence is
CC operatively linked to the promoter in the sense orientation. fda
CC catalyses the conversion of triosephosphate into fructose-1,6
CC bisphosphate in plant chloroplasts (starch synthesis) and in the cytosol
CC (sucrose synthesis). The recombinant DNA vector of the invention is
CC useful for producing genetically transformed plants that have elevated
CC carbon assimilation, storage, export and improved uniformity of solids
CC (e.g. in transgenic potatoes expressing fda). The vector of the invention
CC is particularly useful in the commercial production of foods derived from
CC potatoes which are useful for producing French fries. The transgenic
CC plants exhibit increased photosynthesis rate, increased plant yield,
CC increased growth rate and increased solids uniformity compared with
CC plants that do not contain the recombinant DNA vector. The recombinant
CC DNA vector provides higher quality, more uniform potato tuber regions,
CC and therefore french fries. This results in a higher throughput in the
CC french fry processing plant due to lower processing times, and processor
CC cost savings due to lower energy input required for lower blanch, dry,
CC and par-fry times. The present sequence represents a plant transformation
CC vector containing the E. coli fda gene
XX
SQ Sequence 10900 BP; 2691 A; 2749 C; 2695 G; 2765 T; 0 U; 0 Other;

Query Match 18.5%; Score 310; DB 6; Length 10900;
Best Local Similarity 100.0%; Pred. No. 7.4e-28;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTGTGTAGTTGTACCAATTATGCTTATCTACTA 60
Db |||||||
2059 TGACCGAAGTTAATATGAGGAGTAAACACCTGTGTAGTTGTACCAATTATGCTTATCTACTA 2118
QY 61 GGCACAAATATATTTTTCAGACCTAGAAAAGCTGCAATGTACTGAATACAAAGTATGTC 120
Db |||||||
2119 GGCACAAATATATTTTTCAGACCTAGAAAAGCTGCAATGTACTGAATACAAAGTATGTC 2178
QY 121 CTCCTGTGTTTACACATTTATGACCTTCTTATGTTATTTTCCAGATCTCTGTGCAG 180
Db |||||||
2179 CTCCTGTGTTTACACATTTATGACCTTCTTATGTTATTTTCCAGATCTCTGTGCAG 2238
QY 181 ATTCCTAATCATGCTTTTATATATATAGTTATCTACTCATGGATTTGTAGTTCAGTATGAAA 240
Db |||||||
2239 ATTCCTAATCATGCTTTTATATATATAGTTATCTACTCATGGATTTGTAGTTCAGTATGAAA 2298
QY 241 TATTTTAAATGCAATTTTATGACTTGCCTGCAATTTGATTCGACCAATGCAATGCACTGC 300
Db |||||||
2299 TATTTTAAATGCAATTTTATGACTTGCCTGCAATTTGATTCGACCAATGCAATGCACTGC 2358
QY 301 AGGCACCTCGA 310
Db |||||||
2359 AGGCACCTCGA 2368

RESULT 12

ADQ13598
ID ADQ13598 standard; DNA; 11606 BP.
XX
AC ADQ13598;
XX
DT 23-SEP-2004 (first entry)
XX
DE Plasmid pLBS107 expressing mutant ethylene receptor etr-1.
XX
KW Cotton; ethylene receptor; ds; ethylene insensitivity;
KW abscission zone tissue; plant; transgenic; flower drop; fruit drop;
KW leaf drop; EIN; ethylene insensitive; EIL; ethylene insensitive-like;
KW chitinase; cellulase; polygalacturonase; pLBS107; cyclic; circular.
XX
OS *Gossypium hirsutum*.
OS *Arabidopsis thaliana*.
OS Synthetic.
XX
XX Key Location/Qualifiers
XX CDS 1674..3890
XX /*cag= a
XX /product= "mutant ethylene receptor etr-1"
XX
XX US2004128719-A1.
XX
PD 01-JUL-2004.
XX
XX 23-JUN-2003; 2003US-00602475.
XX
XX 21-JUN-2002; 2002US-0390385P.
XX
XX (KLEE/) KLEE H J.
XX (LASH/) LASHBROOK C.
XX (SHRO/) SHRODE L.
XX
XX Klee HJ, Lashbrook C, Shrode L;
XX
XX WPI; 2004-533137/51.
XX
XX New polynucleotide encoding a mutant plant ethylene receptor protein,
XX useful in decreasing flower, fruit, or leaf drop in a plant upon exposure
XX to ethylene.
XX
XX Example 2; SEQ ID NO 9; 59pp; English.
XX
XX The invention relates to a new polynucleotide comprising (i) a nucleotide
XX sequence encoding a mutant plant ethylene receptor protein, or its
XX fragment, which exhibits ethylene insensitivity, and (ii) a regulatory
XX nucleotide sequence operably linked to the protein encoding nucleotide
XX sequence, where the regulatory nucleotide sequence promotes transcription
XX of the protein encoding nucleotide sequence in cells that comprises
XX abscission zone tissue of a plant. Also included are a cell transformed
XX with the polynucleotide, a plant, plant tissue, or a plant cell
XX transformed with or bred to contain the polynucleotide and a method for
XX decreasing flower, fruit, or leaf drop in a plant upon exposure to
XX ethylene, comprises introducing the polynucleotide into a plant. The
XX polynucleotide preferably comprises a nucleotide sequence encoding a
XX plant EIN (ethylene insensitive), EIL (ethylene insensitive-like) gene
XX product or a mutant ethylene receptor protein is (etr1, etr2, ers1, ers2,
XX or ein4 mutant receptors). The regulatory nucleotide sequence comprises a
XX promoter sequence from a plant chitinase, cellulase, or polygalacturonase
XX gene. The polynucleotide, protein, and method are useful in decreasing
XX flower, fruit, or leaf drop in a plant upon exposure to ethylene. The
XX present sequence represents plasmid pLBS107 expressing mutant ethylene
XX receptor etr-1 from the cotton chitinase promoter.
XX
SQ Sequence 11606 BP; 3014 A; 2696 C; 2782 G; 3113 T; 0 U; 1 Other;

Query Match 18.5%; Score 310; DB 12; Length 11606;
Best Local Similarity 100.0%; Pred. No. 7.3e-28;


```
PF 07-MAY-2002; 2002WO-US014481.
XX
XX
XX 07-MAY-2001; 2001US-0289315P.
XX (POLS/) POLSTON J E.
XX (HIEB/) HIEBERT E.
XX
XX Polston JE, Hiebert E;
XX
XX WPI; 2003-120538/11.
XX
XX Providing resistance to infection by a tomato yellow leaf curl virus in a
XX plant or plant tissue comprises transforming the plant or plant tissue
XX with a polynucleotide.
XX
XX Disclosure; Page 40-41; 41pp; English.
XX
XX The present sequence is the nucleotide sequence of an expression cassette
XX in pKYLX71:35S2. The promoter in this plasmid is a 35S promoter modified
XX by a duplicated enhancer region. The invention provides a means for
XX producing virus resistance in tomato and other crops to infection by
XX tomato yellow leaf curl virus-Israel (TYLCV-Is). A claimed method of
XX providing resistance in a plant involves transforming the plant with a
XX polynucleotide comprising a fragment of a TYLCV Rep gene, a
XX polynucleotide antisense to the truncated Rep gene, or a polynucleotide
XX that hybridizes to the truncated Rep gene or antisense sequence. The
XX plant is selected from statue, petunia, lisianthus, tomatillo, and
XX especially tomato or tobacco, and transformation is performed by
XX agroinfection, biolistic targetting, electroporation or direct gene
XX injection. (Updated on 27-OCT-2003 to standardise OS field)
XX
XX Sequence 1998 BP; 625 A; 411 C; 408 G; 554 T; 0 U; 0 Other;
XX
XX
XX Query Match 17.6%; Score 295; DB 8; Length 1998;
XX Best Local Similarity 100.0%; Pred. No. 5.6e-26;
XX Matches 295; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTGTGACCATTTGCTTATTCACCTA 60
XX
XX 1703 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTGTGACCATTTGCTTATTCACCTA 1762
XX
XX
XX 61 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120
XX
XX 1763 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 1822
XX
XX 121 CTCCTGTGTTTATGACATTTATGAACTTTCCTTTATGTTTATGTTTCCAGATCCTTCTCAG 180
XX
XX 1823 CTCCTGTGTTTATGACATTTATGAACTTTCCTTTATGTTTATGTTTCCAGATCCTTCTCAG 1882
XX
XX
XX 181 ATTCTAATCATTCCTTTATATATATATATATATATATATATATATATATATATATATATAT 240
XX
XX 1883 ATTCTAATCATTCCTTTATATATATATATATATATATATATATATATATATATATATATAT 1942
XX
XX
XX 241 TATTTTTTAATGCAATTTATGATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 295
XX
XX 1943 TATTTTTTAATGCAATTTATGATTCGCAATTCGCAATTCGCAATTCGCAATTCGCAATTCGCA 1997
XX
XX
XX RESULT 15
XX ABV75876
XX ID ABV75876 standard; DNA; 12304 BP.
XX
XX AC ABV75876;
XX
XX
XX 05-FEB-2003 (first entry)
XX
XX Luciferase expression vector ACT-OM-LUC.
XX
XX Vector; ACT-OM-LUC; transgenic plant; bioluminescence; luminescence;
XX firefly; luciferase; enzyme; plant; gene; ds.
XX
XX Photinus; sp.
XX
XX Tobacco mosaic virus.
XX
XX
XX Unidentified.
XX Chimeric.
XX
XX Key Location/Qualifiers
XX misc_feature 6..3450
XX /tag= a
XX /note= "region specifically referred to in Claim 21"
XX enhancer 6..1145
XX /tag= b
XX /note= "actin 2 enhancer and promoter"
XX enhancer 1167..1235
XX /tag= c
XX /note= "tobacco mosaic virus omega translational
XX enhancer"
XX CDS 1243..2895
XX /tag= d
XX /product= "Luciferase"
XX polyA_site 2929..3570
XX /tag= e
XX /note= "Rbcs E9 polyA region"
XX
XX WO200281647-A2.
XX
XX 17-OCT-2002.
XX
XX 08-APR-2002; 2002WO-US011116.
XX
XX 06-APR-2001; 2001US-0282094P.
XX
XX (SCRI ) SCRIPPS RES INST.
XX
XX Kay SA, Kuhlmann T, Lerner RA;
XX
XX WPI; 2003-058526/05.
XX
XX Novel genetically modified plant cell, useful as research tool, comprises
XX a heterologous nucleotide sequence encoding a bioluminescent polypeptide
XX expressed in an amount sufficient to produce visible light.
XX
XX Claim 21; Page 90-96; 96pp; English.
XX
XX The present sequence is that of luciferase expression vector ACT-OM-LUC
XX comprising an expression construct composed of an actin 2 regulatory
XX element comprising an enhancer and promoter, a tobacco mosaic virus omega
XX translational enhancer, a nucleotide sequence encoding luciferase, and an
XX Rbcs E9 polyA region. Claimed vectors, including ACT-OM-LUC, can be used
XX to transform a plant cell such that the cell expresses luciferase in an
XX amount sufficient to produce at least 750,000 photons of visible light/sq
XX mm/second. Also claimed are visibly bioluminescent transgenic plants that
XX contain the genetically modified plant cell. The transgenic plant may be
XX a monocot or dicot, including an angiosperm, cereal, legume, oilseed
XX plant or hardwood tree, or an ornamental plant such as petunia or
XX carnation (all claimed). The transgenic plants are useful as research
XX tools and have ornamental value
XX
XX Sequence 12304 BP; 2928 A; 3115 C; 3142 G; 3119 T; 0 U; 0 Other;
XX
XX
XX Query Match 17.3%; Score 289; DB 8; Length 12304;
XX Best Local Similarity 100.0%; Pred. No. 1.9e-25;
XX Matches 289; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTGTGACCATTTGCTTATTCACCTA 60
XX
XX 3280 TGACCGAAGTTAATATGAGGAGTAAACACCTTGAGTGTGACCATTTGCTTATTCACCTA 3339
XX
XX
XX 61 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 120
XX
XX 3340 GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTACTGAATACAAAGTATGTC 3399
XX
XX
XX 121 CTCCTGTGTTTATGACATTTATGAACTTTCCTTTATGTTTATGTTTCCAGATCCTTCTCAG 180
XX
XX 3400 CTCCTGTGTTTATGACATTTATGAACTTTCCTTTATGTTTATGTTTCCAGATCCTTCTCAG 3459
XX
```

Qy	181	ATTCTAATCATTCGCTTTTATAATTATAGTTTATCTCATGGATTGTAGTTGAGTATGAAAA	240
Db	3460	ATTCTAATCATTCGCTTTTATAATTATAGTTTATCTCATGGATTGTAGTTGAGTATGAAAA	3519
Qy	241	TATTTTTTAATGCATTTTATGACTTGCCCAATTGATTGACACACATGCATC	289
Db	3520	TATTTTTTAATGCATTTTATGACTTGCCCAATTGATTGACACACATGCATC	3568

Search completed: March 31, 2006, 06:51:52
Job time : 1110.43 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:33:28 ; Search time 7670.01 Seconds
(without alignments)
10217.511 Million cell updates/sec

Title: US-10-541-346-4
Perfect score: 1675
Sequence: 1 tgaccgaagttaatatgagg.....tagttcgaaaccttgagaag 1675

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	280	16.7	815	10	ATH517160
2	280	16.7	865	10	AJ517094 Arabidops
3	280	16.7	956	10	ATH516972 Arabidops
4	277.4	16.6	1146	10	AJ517056 Arabidops
5	258.4	15.4	863	10	ATH517085 Arabidops
6	256	15.3	796	10	ATH517067 Arabidops
7	256	15.3	1601	10	ATH517045 Arabidops
8	221.2	13.2	808	10	ATH517113 Arabidops
9	218.4	13.0	970	10	ATH516966 Arabidops
10	201	12.0	975	10	ATH516980 Arabidops
11	169.8	10.1	1896	10	CG753083 Arabidops
12	169	10.1	1313	7	CK997149 Arabidops
13	164.2	9.8	1896	10	CG753083 Arabidops
14	162.6	9.7	1227	10	AG430010 Arabidops
15	162.2	9.7	820	10	ATH517144 Arabidops
16	162.2	9.7	1277	9	CC253231 Arabidops
17	161.2	9.6	1238	1	AJ925855 Arabidops
18	160.8	9.6	1359	8	DN685273 Arabidops
19	160.6	9.6	1202	9	CC262481 Arabidops
20	156.2	9.3	1542	10	AG386981 Arabidops
21	155.2	9.3	1392	10	CG757503 Arabidops
22	154	9.2	1391	10	CG754863 Arabidops

23 153.4 9.2 1189 1 AJ925925
24 153 9.1 1313 7 CK997149
25 152.8 9.1 1592 10 CG750135
26 152.6 9.1 1211 10 AG349657 Mus muscu
27 152 9.1 817 10 ATH516963
28 151.6 9.1 1101 10 CNS0021J
29 151.6 9.1 1325 10 CW952344
30 151.4 9.0 1268 10 AG347098
31 151.2 9.0 1242 10 CL068807
32 150.8 9.0 1101 10 CNS008VL
33 150.4 9.0 1489 10 AG350139
34 150 9.0 1378 10 AG350209 Mus muscu
35 149.8 8.9 1489 10 AG350139
36 149 8.9 976 10 CW949642
37 149 8.9 1539 10 AG340947
38 148.4 8.9 991 10 CL139092
39 148.4 8.9 1608 10 CL118721
40 148.2 8.8 1092 1 AJ927993
41 147.2 8.8 1254 10 AG349719
42 146.8 8.8 1359 8 DN685273
43 146.4 8.7 1275 10 CL033318
44 146.4 8.7 1364 10 CG757986
45 146.2 8.7 939 5 BY720774

ALIGNMENTS

RESULT 1
ATH517160
LOCUS Arabidopsis thaliana GSS, clone 22B/77, DNA linear GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/77, genomic survey sequence.
ACCESSION AJ517160
VERSION AJ517160.1 GI:25252960
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 815)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL Collection (AATSTC)
REFERENCE 2 (bases 1 to 815)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES
source
1..815
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="22B/77"
/ecotype="Columbia"

ORIGIN

Query Match 16.7%; Score 280; DB 10; Length 815;
Best Local Similarity 100.0%; Pred. No. 3.2e-29;
Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 319 CTCATCTAGCCCCCATTGGAGCTGAATGTAGACACGTGCGAATAAGATTTCCGAATT 378
DB 153 CTCATCTAGCCCCCATTGGAGCTGAATGTAGACACGTGCGAATAAGATTTCCGAATT 212
QY 379 AGAATAATTGTTTATGTTTCCTTATTAATACACCGATCGTAATTTGTCGTTTAT 438
DB 213 AGAATAATTGTTTATGTTTCCTTATTAATACACCGATCGTAATTTGTCGTTTAT 272
QY 439 CAAATGTAATTTTATTAATTAATACGCTGCGGACATCTACATTTTGAATTTGAAAAA 498

Db 273 CAAATGTACTTTCTTTTATAATAACGCTGGGACATCTACATTTTGAATTGAAAAA 332
 QY 499 AATTGTAATTAATCTTTCTTTTCTCCATATTGACCATCACTACATTTGCTGATCCATG 558
 Db 333 AATTGTAATTAATCTTTCTTTTCTCCATATTGACCATCACTACATTTGCTGATCCATG 392
 QY 559 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 598
 Db 393 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 432

RESULT 2

ATH517094/c
 LOCUS Arabidopsis thaliana GSS, clone 22B/469, genomic survey sequence.
 DEFINITION Arabidopsis thaliana GSS, clone 22B/469, genomic survey sequence.
 ACCESSION AJ517094

VERSION AJ517094.1 GI:25252831

KEYWORDS GSS; genome survey sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 865)

AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
 TITLE An Arabidopsis promoter activation-tagged flanking sequence
 JOURNAL collection (AATSTC)

UNPUBLISHED

REFERENCE 2 (bases 1 to 865)

AUTHORS Reiss,B.

TITLE Direct Submission

JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding

Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany

FEATURES

source Location/Qualifiers

1..865

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="22B/469"

/ecotype="Columbia"

ORIGIN

Query Match 16.7%; Score 280; DB 10; Length 865;
 Best Local Similarity 100.0%; Pred. No. 3.2e-29;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378

Db 403 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 344

QY 379 AGAATAATTTGTTTATGCTTTTCGCCCTATAAATACACGGATCGTAATTTGCTGTTTTAT 438

Db 343 AGAATAATTTGTTTATGCTTTTCGCCCTATAAATACACGGATCGTAATTTGCTGTTTTAT 284

QY 439 CAAAATGTAATTTCAATTTTATATACGCTGGGACATCTACATTTTTCGAATTGAAAAA 498

Db 283 CAAAATGTAATTTCAATTTTATATACGCTGGGACATCTACATTTTTCGAATTGAAAAA 224

QY 499 AATTGTAATTAATCTTTCTTTTCTCCATATTGACCATCACTACATTTGCTGATCCATG 558

Db 223 AATTGTAATTAATCTTTCTTTTCTCCATATTGACCATCACTACATTTGCTGATCCATG 164

QY 559 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 598

Db 163 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 124

RESULT 3

ATH516972/c

LOCUS

DEFINITION Arabidopsis thaliana GSS, clone 22B/658, genomic survey sequence.

ACCESSION AJ516972

VERSION AJ516972.1 GI:25252596

KEYWORDS

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 956)

AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
 TITLE An Arabidopsis promoter activation-tagged flanking sequence
 JOURNAL collection (AATSTC)

UNPUBLISHED

REFERENCE 2 (bases 1 to 956)

AUTHORS Reiss,B.

TITLE Direct Submission

JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding

Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany

FEATURES

source

1..956

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="22B/658"

/note="ecotype: Columbia"

ORIGIN

Query Match 16.7%; Score 280; DB 10; Length 956;
 Best Local Similarity 100.0%; Pred. No. 3.1e-29;
 Matches 280; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 319 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378

Db 291 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 232

QY 379 AGAATAATTTGTTTATGCTTTTCGCCCTATAAATACACGGATCGTAATTTGCTGTTTTAT 438

Db 231 AGAATAATTTGTTTATGCTTTTCGCCCTATAAATACACGGATCGTAATTTGCTGTTTTAT 172

QY 439 CAAAATGTAATTTCAATTTTATATACGCTGGGACATCTACATTTTTCGAATTGAAAAA 498

Db 171 CAAAATGTAATTTCAATTTTATATACGCTGGGACATCTACATTTTTCGAATTGAAAAA 112

QY 499 AATTGTAATTAATCTTTCTTTTCTCCATATTGACCATCACTACATTTGCTGATCCATG 558

Db 111 AATTGTAATTAATCTTTCTTTTCTCCATATTGACCATCACTACATTTGCTGATCCATG 52

QY 559 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 598

Db 51 TAGATTTCCGGACATGAAGCCATTTACAAATTGAATATAT 12

RESULT 4

ATH517056

LOCUS

DEFINITION Arabidopsis thaliana GSS, clone 22B/820, genomic survey sequence.

ACCESSION AJ517056

VERSION AJ517056.1 GI:25252758

KEYWORDS GSS; genome survey sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1146)

AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
 TITLE An Arabidopsis promoter activation-tagged flanking sequence
 JOURNAL collection (AATSTC)

UNPUBLISHED

REFERENCE 2 (bases 1 to 1146)

AUTHORS Reiss,B.

TITLE Direct Submission

JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding

Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany

FEATURES

Location/Qualifiers

```
source 1. .1146
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="22B/820"
/ecotype="Columbia"

ORIGIN
Query Match 16.6%; Score 277.4; DB 10; Length 1146;
Best Local Similarity 91.8%; Pred. No. 6.9e-29;
Matches 293; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 319 CTCATCTAAGCCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378
DB 65 CTCATCTAAGCCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 124

QY 379 AGAATAAATTTGTTTATTTGCTTTTCGCCCTATAAATACGCGATCTACATTTTGAATTTGAAATTTG 438
DB 125 AGAATAAATTTGTTTATTTGCTTTTCGCCCTATAAATACGCGATCTACATTTTGAATTTGCTTTTAT 184

QY 439 CAAATGTACTTTCTTTTATTAATAAGCGTTCGCCGACATCTACATTTTGAATTTGAAAAA 498
DB 185 CAAATGTACTTTCTTTTATTAATAAGCGTTCGCCGACATCTACATTTTGAATTTGAAAAA 244

QY 499 AATGGTAATTAATCTTTCTTTTTCCTCATATTGACATCAATCTCATTTGCTGATCCATG 558
DB 245 AATGGTAATTAATCTTTCTTTTTCCTCATATTGACATCAATCTCATTTGCTGATCCATG 304

QY 559 TAGATTCCCGGACATGAAGCCATTTTACATTTGAATTAATATATTTACAAGCTATTTGCTTA 618
DB 305 TAGATTCCCGGACATGAAGCCATTTTACATTTGAATTAATATATTTACAAGCTATTTGCTTA 364

QY 619 TAACATATGCGAAAAATTT 637
DB 365 TATCTTCGCAAGACCTT 383

RESULT 5
ATHS17085/c
LOCUS ATHS17085 863 bp DNA linear GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/472, genomic survey sequence.
ACCESSION AJ517085
VERSION AJ517085.1 GI:25252813
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 863)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 863)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES
source
1. .863
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="22B/472"
/ecotype="Columbia"

ORIGIN
Query Match 15.4%; Score 258.4; DB 10; Length 863;
Best Local Similarity 97.2%; Pred. No. 3e-26;
Matches 274; Conservative 0; Mismatches 6; Indels 2; Gaps 1;

QY 319 CTCATCTAAGCCCCCATTTGGAGCGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378
```

Db 314 TAGATTTCCTGACGAGAACCAACCGCTTTGAAATCGAAACAGACAGATATCATCA 373
QY 619 TAAC 622
Db 374 GAAC 377

RESULT 7
ATH517045
LOCUS Arabidopsis thaliana 1601 bp DNA linear GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/83, genomic survey sequence.
ACCESSION AJ517045
VERSION AJ517045.1 GI:25252736
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1601)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL collection (AATSTC)
REFERENCE 2 (bases 1 to 1601)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES
source
1..1601
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="22B/83"
/ecotype="Columbia"

ORIGIN
Query Match 15.3%; Score 256; DB 10; Length 1601;
Best Local Similarity 90.1%; Pred. No. 5.8e-26;
Matches 274; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 319 CTCATCTAGAGCCCCCATTTGGAGCGTAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378
Db 74 CTCATCTAGAGCCCCCATTTGGAGCGTAATGTAGACACGTCGAAATAAAGATTTCCGAATT 133

QY 379 AGAATAATTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGTCGTTTTAT 438
Db 134 AGAATAATTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGTCGTTTTAT 193

QY 439 CAAAATGTACTTTTATTAATAACGCTGCGGACATCTACATTTTGAATTGAAAAA 498
Db 194 CAAAATGTACTTTTATTAATAACGCTGCGGACATCTACATTTTGAATTGAAAAA 253

QY 499 AATTGGTAATTAATCTCTTTTCTCCATATTGACCATCATCTATTGCTGATCCATG 558
Db 254 AATTGGTAATTAATCTCTTTTCTCCATATTGACCATCATCTATTGCTGATCCATG 313

QY 559 TAGATTTCGGACATGAAGCCATTTTACAAATGAATATATATTACAAAGCTATTTGCTTAA 618
Db 314 TAGATTTCCTGACGAGAACCAACCGCTTTGAAATCGAAACAGACAGATATCATCA 373

QY 619 TAAC 622
Db 374 GAAC 377

RESULT 8
ATH517113/c
LOCUS Arabidopsis thaliana 808 bp DNA linear GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/746, genomic survey sequence.
ACCESSION AJ517113
VERSION AJ517113.1 GI:25252867

KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 808)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL collection (AATSTC)
REFERENCE 2 (bases 1 to 808)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES
source
1..808
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="22B/746"
/ecotype="Columbia"

ORIGIN
Query Match 13.2%; Score 221.2; DB 10; Length 808;
Best Local Similarity 80.7%; Pred. No. 4.2e-21;
Matches 226; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 319 CTCATCTAGAGCCCCCATTTGGAGCGTAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378
Db 291 CTCATCTAGAGCCCCCATTTGGANGTGAATGTAGNACGTCGNAATNAAGATTTCCNAATT 232

QY 379 AGAATAATTGTTTATTGCTTTTCGCCTATAAATACGACGGATCGTAATTTGTCGTTTTAT 438
Db 231 AGAANNATNNGTTTATNCTTNGCCTANNAANNCCGCGTNNNNNGTCGNTTTAT 172

QY 439 CAAAATGTACTTTTATTAATAACGCTGCGGACATCTACATTTTGAATTGAAAAA 498
Db 171 CAAAATGAACNTTCNNNTTGAATGACGCGGAGCANNNACAGTTTTGNAITGAAACAC 112

QY 499 AATTGGTAATTAATCTCTTTTCTCCATATTGACCATCATCTATTGCTGATCCATG 558
Db 111 AATTGGNAATTAATCTCTNNCTTTTCTCCATATTGACCATCATCTANTGTCATCATG 52

QY 559 TAGATTTCGGACATGAAGCCATTTTACAAATGAATATAT 598
Db 51 TAGATTTCGCGACATGAAGCCATTTTCAATTNAATATAT 12

RESULT 9
ATH516966/c
LOCUS Arabidopsis thaliana 970 bp DNA linear GSS 12-MAR-2003
DEFINITION Arabidopsis thaliana GSS, clone 22B/774, genomic survey sequence.
ACCESSION AJ516966
VERSION AJ516966.1 GI:25252584
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 970)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
JOURNAL collection (AATSTC)
REFERENCE 2 (bases 1 to 970)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES
Location/Qualifiers

```
source 1. .970
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="22B/774"
/note="ecotype: Columbia"

ORIGIN
Query Match 13.0%; Score 218.4; DB 10; Length 970;
Best Local Similarity 96.4%; Pred. No. 9.8e-21;
Matches 244; Conservative 0; Mismatches 7; Indels 2; Gaps 2;
QY 319 CTGATCTAAGCCCCCATTTGACGTGAATGTAGACACGTCGAAATAAGATTTCCGGAATT 378
Db 260 CTCATCTAAGCCCCCATTTGACGTGAATGTAGACACGTCGAAATAAGATTTCCGGAATT 201
QY 379 AGAATAATTTGTTTATTGCTTTCCGCTATAAATACGACGATCGTAATTTTGTGCTTTTAT 438
Db 200 AGATAATTTGTTTATTGCTTTCCGCTATAAATACGCGATCGTAATTTTGTGCTTTTAT 141
QY 439 CAAAATGACTTTTCATTTTAAATACGCTCGCGACATCTACATTTTGAATTTGAAAAA 498
Db 140 CAAAATG-ACCTTCATTTTAAATACGCTCGCGACATCAACATTTTGAATTTGAAAAA 82
QY 499 AATTGGTAATACT-CTTCTCTTTCTCCATATTGACCATCATCTACTGCTGATCCAT 557
Db 81 AATTGGTAATTAATCTCCCTCTTTTCTCCATATTGACCATCATCTACTGATCCAT 22
QY 558 GTAGATTTCCGG 570
Db 21 GTAGATTTCTGG 9

RESULT 10
ATH516980/c 975 bp DNA linear GSS 12-MAR-2003
LOCUS Arabidopsis thaliana GSS, clone 22B/557, genomic survey sequence.
DEFINITION
ACCESSION AJ516980
VERSION AJ516980.1 GI:25252612
KEYWORDS GSS; genome survey sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 975)
AUTHORS Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE An Arabidopsis promoter activation-tagged flanking sequence
collection (AATSTC)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 975)
AUTHORS Reiss,B.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES
source
1. .975
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="22B/557"
/note="ecotype: Columbia"

ORIGIN
Query Match 12.0%; Score 201; DB 10; Length 975;
Best Local Similarity 87.4%; Pred. No. 2.5e-18;
Matches 236; Conservative 0; Mismatches 31; Indels 3; Gaps 2;
QY 320 TCATCTAAGCCCCCATTTGACGTGAATGTAGACACGTCGAAATAAGATTTCCGGAATTA 379
Db 277 TCATNTAAGCCCCCATTTGACGTGAATGTAGAAACGTCNNAATAAGATTTCCGGAATTA 218
QY 380 GAATAATTTGTTTATTGCTTTCCGCTATAAATACGACGATCGTAATTTTGTGCTTTTAA-- 437

source 1. .1896
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Ppa EcoRI BAC Library"
/note="The library was generated by a partial digest of
the genomic DNA with EcoRI and cloning into the BAC
vector."

ORIGIN
Query Match 10.1%; Score 169.8; DB 10; Length 1896;
Best Local Similarity 50.2%; Pred. No. 4.4e-14;
Matches 457; Conservative 0; Mismatches 449; Indels 4; Gaps 3;
QY 693 AAATGAAAAAATTTCTTATTAGTTATTTAAAAATTTTAAAGTAAAAATATAAAATTTTCAT 752
Db 250 ATATTTTATTTATTTAATAATAAATAATATATATATATATATATATATATATATATATAT 309
QY 753 TTAATCCTTTAAATATATAAGATAT-AGACTATTAAATATGATGAAATACAAATTTTAT 811
Db 310 TTATTTATTTATATATATATATATATATATATATATATATATATATATATATATATAT 369
QY 812 TATCATATAAATATATAATTTAAATTTTCGACCCCTAACAAAAATTTTCGATTTTCCCTCAA 871
Db 370 TATTAATAAATATAAATTTTATTAATAATTAATAATNATTTTATAATTAATAATAATA 429
QY 872 CTGTATATTTGTATATAAACAATTTTCTTTTTCATTTTAAATGATTTCTTTTAAATTCAGTCC 931
```

Db 430 TATTATTATTATTAATAAAAAATATAATAAATATTTAATAATAATAATAATAATTTAATAATNT 489
 QY 932 AAGAAAGAAATTTATTAATGATATGCGAAGTAGTCTTGCCTAGTGATATTAAGG 991
 Db 490 ATAATAAATATTAATAAATAAATTTATATAAATTTTATATAATTTATATAATTAATAATATA 549
 QY 992 AAGAAACATAAAATCAATAAATAATTTTAAAGCAATAGTAAATAAAGCAAAACT 1051
 Db 550 TATATATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 609
 QY 1052 TTCTACGATGCTATTAATTTCAAAAAAGAAATAAATCTTTAAACCAATGAATTTAAA 1111
 Db 610 TTTTAAATAATNATAAATTTTATAAATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 669
 QY 1112 ATACATCAGATATCTATTTATTTAATTTAATAAATAAATAAATAAATAAATAAATAAATAA 1171
 Db 670 ATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 729
 QY 1172 TTAATAATTTTATTTAGCTTAGTGTCACAAATCAATAAATAAATAAATAAATAAATAAATAA 1231
 Db 730 TTAATAAATTTATTAATTTATTAATTTATTAATTTATTAATTTATTAATTTATTAATTTATTA 789
 QY 1232 ATATATATTTTGAGGGTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1291
 Db 790 ATTATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 849
 QY 1292 ATACACATATAAATAATTTGAATCCAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1350
 Db 850 TTTTATTTTNTATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT 909
 QY 1351 CAACCAAAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 1410
 Db 910 AATAATTTAATTTTAAATTTAATAAATAAATTTAATTTAATAAATAAATTTAATTTAATAAATA 969
 QY 1411 CGATTTTTTTTACCTA--TATATAGATGACATAATCTACTTTAAATTTAAATTTAAATTTAAAT 1468
 Db 970 ATAAATAAATAATNTATTTATTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 1029
 QY 1469 ATATATATACACAAAAAATTTCTTAAATGATCTGATAAATCTTAAATTTAAATTTAAATTTAA 1528
 Db 1030 AATATATAAANAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1089
 QY 1529 AACAATCTTAACCCCTTATATTTTAAATTTAATAATCATTTAATAAATAAATAAATAAATAA 1588
 Db 1090 TTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1149
 QY 1589 GCATATGTTT 1598
 Db 1150 TTTTATTTAT 1159

RESULT 12

CK997149

LOCUS

DEFINITION CK997149 1313 bp mRNA linear EST 26-MAR-2004
 ip15c02.b1 Brain - Cerebellum Library (DOEST8) Canis familiaris
 CDNA clone ip15c02, mRNA sequence.

ACCESSION

CK997149

VERSION

CK997149.1

KEYWORDS

EST.

SOURCE

Canis familiaris (dog)

ORGANISM

Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;

Canis.

REFERENCE

1 (bases 1 to 1313)

Ballia V., Nascimento, L.U. and McCombie, W.R.

ESTs from Canis familiaris cerebellum (dog)

Unpublished (2004)

Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8884

FEATURES

source

Fax: 516 367 8874
 Email: mcombie@cshl.org
 Plate: ip15 row: C column: 02
 High quality sequence scop: 1313.
 Location/Qualifiers
 1..1313
 /organism="Canis familiaris"
 /mol_type="mRNA"
 /db_xref="taxon:9615"
 /clone="ip15c02"
 /sex="Unknown"
 /tissue type="Cerebellum"
 /dev stage="3 month old normal canine"
 /lab_host="XL10 Gold"
 /clone_lib="Brain - Cerebellum Library (DOEST8)"
 /note="Organ: Brain; Vector: pBluescript II SK; Site 1:
 XR kit; Site 2: XhoI; Library constructed using pluescript
 XR kit from Stratagene. Cloned cDNA was size selected
 between 1-3 kb. Mark Haskins VMD, PhD, Pathology and
 Medical Genetics, School of Veterinary Medicine,
 University of Pennsylvania, 3800 Spruce Street,
 Philadelphia, PA 19104-6051"

ORIGIN

Query Match 10.1%; Score 169; DB 7; Length 1313;
 Best Local Similarity 49.1%; Pred. No. 6e-14;
 Matches 571; Conservative 0; Mismatches 566; Indels 25; Gaps 5;
 QY 426 TTTGCTGTTTATCAAAATGTACTTTTCATTTTATTAATAACGCTCGGACATCTCACATTTT 485
 Db 162 TTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 221
 QY 486 TGAATGAAAAAATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 545
 Db 222 AAAATAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 281
 QY 546 TTGCTGATCCATGATGATTTCCGGACATGAAGCCATTTACAAATGGAATATATATATACAA 605
 Db 282 TATATAATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 341
 QY 606 AGCTATTTGCTTTATACATATATCGAAAAATTTTGTACTATAATCAGGGGTAAATTTTGGGA 665
 Db 342 TTTTATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 401
 QY 666 GGGGCTGTAGGTCTCGCTTCTTAAATGAAAAATTTTCTATTTAGTATTTAAAAAT 725
 Db 402 AATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 453
 QY 726 TTTAAAAAGTAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 785
 Db 454 ATTATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 513
 QY 786 TTTAAATGATGAAATTTACAAATTTTATTTATCATAAAAATTTAATTTAATTTTCGACCCCTA 845
 Db 514 ATATATATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 573
 QY 846 ACAAAATTTCTGATTTTTCGCCCTCACTGATAATTTGTATATAAACAATTTTCTTTTTCG 905
 Db 574 AAAAAATTTTNTTATTTTAAATTTAAATAATATATATAAATAAATAAATAAATAAATAAATA 633
 QY 906 ATTTAATGATTTCTTTAATTTCAAGCAAGAAAGAAATTTTAAATTTGCATATGCGAAAGT 965
 Db 634 AAAAAATAAATTTTAAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 693
 QY 966 TAGTCTTCTGCTAGTATTAATAAGGAAAGAAACAT-----AAAAATAAATAAATAAATAA 1018
 Db 694 AATTTTATATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 753
 QY 1019 TTTTAAAGCAATAGTAAATAAATAAAGGAAAACTTTCTCAGTAGTCTATAATTTCAAAAAA 1078
 Db 754 TTTTATTTATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 813
 QY 1079 AGAATAATAAATCTTTTAAACCATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATA 1138


```

RESULT 15
ATH517144
LOCUS      ATH517144      820 bp      DNA      linear      GSS 22-NOV-2002
DEFINITION Arabidopsis thaliana GSS, clone 22B/398, genomic survey sequence.
ACCESSION  AJ517144
VERSION     AJ517144.1  GI:25252928
KEYWORDS    GSS; genome survey sequence.
SOURCE      Arabidopsis thaliana (thale cress)
ORGANISM    Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1 (bases 1 to 820)
AUTHORS     Ichikawa,T., Rosso,M., Werber,M., Dekker,K., Schell,J. and Reiss,B.
TITLE       An Arabidopsis promoter activation-tagged flanking sequence
            collection (AATSTC)
JOURNAL      Unpublished
REFERENCE   2 (bases 1 to 820)
AUTHORS     Reiss,B.
TITLE       Direct Submission
JOURNAL      Submitted (14-NOV-2002) Max Planck Institute for Plant Breeding
            Research, Carl-von-Linne-Weg 10, Koeln 50829, Germany
FEATURES    source
            1..820
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /db_xref="taxon:3702"
            /clone="22B/398"
            /ecotype="Columbia"

ORIGIN
Query Match      9.7%; Score 162.2; DB 10; Length 820;
Best Local Similarity 92.6%; Pred. No. 5.7e-13; Mismatches 13; Indels 3; Gaps 3;
Matches 200; Conservative 0;

QY 319 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCGGAATT 378
Db 598 CTCATCTAAGCCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCGCAATT 657
QY 379 AGAATAAATTGTTTATTCG- TTTCGCCTATAAATACGACGGATCGTAATT- GTCGTTTT 436
Db 658 AGAATAAATTGTTTATTCG- TTTCGCCTATAAATACGACGGATCGTAATT- GTCGTTTT 717
QY 437 ATCAAAATGCTCTTTTCATTTTATAATAA- CGCTGCGGACATCTACATTTTGAATTGAAA 495
Db 718 ATCAAAATGCTCTTTTCATTTTATAATAA- CGCTGCGGACATTTACATTTTGAATTGGAA 777
QY 496 AAAAAATTGTAATTACTCTTTCTTTTCTCCATATT 531
Db 778 AAAAAATTGGAATTACTCTTTCTTTTCTCTCTNAT 813

```

Search completed: March 31, 2006, 12:24:23
 Job time : 7674.01 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 30, 2006, 14:04:38 ; Search time 552.987 Seconds
(without alignments)
5384.242 Million cell updates/sec

Title: US-10-541-346-4

Perfect score: 1675

Sequence: 1 tgaccgaagtaatatgagg.....tagtgcgaacctggagaag 1675

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq.*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/H COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/PTUS COMB.seq.*
- 7: /cgn2_6/ptodata/1/ina/PP COMB.seq.*
- 8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
- 9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	310	18.5	8012	3	US-09-182-117-1
2	310	18.5	8012	3	US-09-434-039A-1
3	310	18.5	8418	3	US-09-182-117-5
4	310	18.5	8418	3	US-09-434-039A-5
5	310	18.5	8798	3	US-09-182-117-4
6	310	18.5	8798	3	US-09-434-039A-4
7	310	18.5	10846	3	US-09-098-219B-5
8	310	18.5	10846	3	US-10-164-204-5
9	310	18.5	10846	3	US-09-923-109-5
10	310	18.5	10900	3	US-09-098-219B-6
11	310	18.5	10900	3	US-10-164-204-6
12	310	18.5	10900	3	US-09-923-109-6
13	289	17.3	12614	3	US-09-577-424-1
14	282	16.8	632	3	US-10-015-637-7
15	280.2	16.7	7811	2	US-08-549-680A-5
16	280.2	16.7	10249	3	US-09-186-002-14
17	280.2	16.7	10252	3	US-09-186-002-15
18	280.2	16.7	10339	3	US-09-186-002-13
19	280.2	16.7	14194	3	US-09-577-424-3
20	280.2	16.7	15397	2	US-08-673-768-1
21	280.2	16.7	24595	9	5428147-1
22	270.2	16.1	10323	3	US-09-280-428A-11
23	153.2	9.1	187169	3	US-09-949-016-12776
24	153.2	9.1	191569	3	US-09-949-016-15940

ALIGNMENTS

RESULT 1

US-09-182-117-1
; Sequence 1, Application US/09182117
; Patent No. 6204436

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Transgenic Plant

; NUMBER OF SEQUENCES: 27

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25 (BPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/182,117

; FILING DATE:

; CLASSIFICATION:

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 8012 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

US-09-182-117-1

Query Match

Best Local Similarity 18.5%; Score 310; DB 3; Length 8012;

Mismatches 310; Conservative 0; Indels 0; Gaps 0;

QY	1	TGACCAAGCTTATATGAGGAGTAAACACTTCTAGCTGTACCATTTGCTTATTCACCTA	60
Db	2708	TGACCAAGCTTATATGAGGAGTAAACACTTCTAGCTGTACCATTTGCTTATTCACCTA	2767
QY	61	GGCAACAATATATTTTTCAGACCTAGAAAGCTGCAAACTGTACTGTAACAAGTATGTC	120
Db	2768	GGCAACAATATATTTTTCAGACCTAGAAAGCTGCAAACTGTACTGTAACAAGTATGTC	2827
QY	121	CTCTGTGTTTTAGACATTTATGAATTCCTTTATATATTTTCCAGAAATCCTTGTGAG	180
Db	2828	CTCTGTGTTTTAGACATTTATGAATTCCTTTATATATTTTCCAGAAATCCTTGTGAG	2887
QY	181	ATTCTAATCATTCCTTTTATTAATTTATAGTTATATCTCATGGATTTGTAGTATGAAAA	240
Db	2888	ATTCTAATCATTCCTTTTATTAATTTATAGTTATATCTCATGGATTTGTAGTATGAAAA	2947

Matches	310;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	1	TGACCGAAGTTAATATGAGGAGTAAAAACACTTGTAGTGTGACCAATTATGCTTATTCACTA	60						
Db	2687	TGACCGAAGTTAATATGAGGAGTAAAAACACTTGTAGTGTGACCAATTATGCTTATTCACTA	2746						
QY	61	GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGCTTACTGAATACAAAGTATGTC	120						
Db	2747	GGCAACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGCTTACTGAATACAAAGTATGTC	2806						
QY	121	CTCTGTGTTTTAGACATTTTATGAACCTTCCCTTTATGTAAATTTCCAGAAATCCTTGTTCAG	180						
Db	2807	CTCTGTGTTTTAGACATTTTATGAACCTTCCCTTTATGTAAATTTCCAGAAATCCTTGTTCAG	2866						
QY	181	ATTCTAATCAATGCTTTTATAATTTATAGTTATACTCATGGATTTGTAGTTCAGATATGAAAA	240						
Db	2867	ATTCTAATCAATGCTTTTATAATTTATAGTTATACTCATGGATTTGTAGTTCAGATATGAAAA	2926						
QY	241	TATTTTTTAATGCACTTTTATGACTGTGCCAATTGATGTGACCAATGCATCAATCGACTGC	300						
Db	2927	TATTTTTTAATGCACTTTTATGACTGTGCCAATTGATGTGACCAATGCATCAATCGACTGC	2986						
QY	301	AGCCACTCGA	310						
Db	2987	AGCCACTCGA	2996						

```

RESULT 5
US-09-182-117-4
; Sequence 4, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Transgenic Plant
; NUMBER OF SEQUENCES: 27
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/182,117
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8798 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-182-117-4

```

Db	2977	ATTCTAATCATTCGCTTTATTAATATATAGTTTATACTCATGCAATTTGTAGTTGAGTATGAAAA	3036
Qy	241	TATTTTTTAATGCAATTTTATGACTTGCCTCAATTTGATGACAAACATGTCATCAATCGACCTGC	300
Db	3037	TATTTTTTAATGCAATTTTATGACTTGCCTCAATTTGATGACAAACATGTCATCAATCGACCTGC	3096
Qy	301	AGCCACTCGA	310
Db	3097	AGCCACTCGA	3106

RESULT 6
US-09-434-039A-4
; Sequence 4, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
; APPLICANT: MANNERLOEF, Marie
; APPLICANT: TENNING, Paul Peter

```

RESULT 6
US-09-434-039A-4
; Sequence 4, Application US/09434039A
; Patent No. 6531649
; GENERAL INFORMATION:
; APPLICANT: MANNERLOEF, Marie
; APPLICANT: TENNING, Paul Peter
; APPLICANT: STEEN, Per
; TITLE OF INVENTION: Transgenic Plants
; FILE REFERENCE: 09/434,039
; CURRENT APPLICATION NUMBER: US/09/434,039A
; CURRENT FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: 60/112,003
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 09/182,117
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 8798
; TYPE: DNA
; ORGANISM: Sugar beet
US-09-434-039A-4

```

```

RESULT 7
US-09-098-219B-5
; Sequence 5, Application US/09098219B
; Patent No. 6441277
; GENERAL INFORMATION:
; APPLICANT: Barry, Gerard
; APPLICANT: Cheikh, No. 6441277dine
; APPLICANT: Kishore, Ganesh
; TITLE OF INVENTION: Expression of Fructose 1,6 Bispophosphate

```

;; TITLE OF INVENTION: Aldolase in Transgenic Plants
;; NUMBER OF SEQUENCES: 6
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Arnold White & Durkee
;; STREET: P.O. Box 4433
;; CITY: Houston
;; STATE: TX
;; COUNTRY: US
;; ZIP: 77210-4433
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/098,219B
;; FILING DATE:
;; CLASSIFICATION: 800
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/049,995
;; FILING DATE: 17-JUN-1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Kammerer, Patricia A.
;; REGISTRATION NUMBER: 29,775
;; REFERENCE/DOCKET NUMBER: MOBT:086
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 713-787-1400
;; TELEFAX: 713-787-1440
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10846 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
US-09-098-219B-5

Query Match 18.5%; Score 310; DB 3; Length 10846;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGACCATTTGTTTATTCACCTA 60
Db 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGACCATTTGTTTATTCACCTA 2118

QY 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAAATACAAGTATGTC 120
Db 2119 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAAATACAAGTATGTC 2178

QY 121 CTCCTGTGTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180
Db 2179 CTCCTGTGTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 2238

QY 181 ATTCTAATCATGCTTTTATAATTTAGTTATGTTTACTCATGGAATTTAGTTGAGTATGAAA 240
Db 2239 ATTCTAATCATGCTTTTATAATTTAGTTATGTTTACTCATGGAATTTAGTTGAGTATGAAA 2298

QY 241 TATTTTAAATGATTTTATGCTCCCAATTTGATGCAACATGCAATCAATCGACCTGC 300
Db 2299 TATTTTAAATGATTTTATGCTCCCAATTTGATGCAACATGCAATCAATCGACCTGC 2358

QY 301 AGCCACTCGA 310
Db 2359 AGCCACTCGA 2368

RESULT 8
US-10-164-204-5
;; Sequence 5, Application US/10164204
;; Patent No. 6663906
;; GENERAL INFORMATION:
;; APPLICANT: Barry, Gerard
;; APPLICANT: Cheikh, No. 6663906dine
;; APPLICANT: Kishore, Ganesh

;; TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate Aldolase in Transgenic Plants
;; FILE REFERENCE: 11899.0086.DVUS02 (MOBT:086-2)
;; CURRENT APPLICATION NUMBER: US/10/164,204
;; CURRENT FILING DATE: 2002-06-06
;; PRIOR APPLICATION NUMBER: 09/098,219
;; PRIOR FILING DATE: 1998-06-16
;; NUMBER OF SEQ ID NOS: 6
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 5
;; LENGTH: 10846
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: P-FMW/CTPI/fda/NOS3,
US-10-164-204-5

Query Match 18.5%; Score 310; DB 3; Length 10846;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGACCATTTGTTTATTCACCTA 60
Db 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGACCATTTGTTTATTCACCTA 2118

QY 61 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAAATACAAGTATGTC 120
Db 2119 GGCAACAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGAAATACAAGTATGTC 2178

QY 121 CTCCTGTGTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180
Db 2179 CTCCTGTGTTTAGACATTTATGAACTTTCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 2238

QY 181 ATTCTAATCATGCTTTTATAATTTAGTTATGTTTACTCATGGAATTTAGTTGAGTATGAAA 240
Db 2239 ATTCTAATCATGCTTTTATAATTTAGTTATGTTTACTCATGGAATTTAGTTGAGTATGAAA 2298

QY 241 TATTTTAAATGATTTTATGCTCCCAATTTGATGCAACATGCAATCAATCGACCTGC 300
Db 2299 TATTTTAAATGATTTTATGCTCCCAATTTGATGCAACATGCAATCAATCGACCTGC 2358

QY 301 AGCCACTCGA 310
Db 2359 AGCCACTCGA 2368

RESULT 9
US-09-923-109-5
;; Sequence 5, Application US/09923109
;; Patent No. 6716474
;; GENERAL INFORMATION:
;; APPLICANT: Barry, Gerard
;; APPLICANT: Cheikh, No. 6716474dine
;; APPLICANT: Kishore, Ganesh
;; TITLE OF INVENTION: Expression of Fructose 1,6 Bisphosphate
;; Aldolase in Transgenic Plants

NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICANT NUMBER: US/09/923,109
FILING DATE: 06-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/098,219
FILING DATE: <Unknown>
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10846 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-923-109-5
Query Match 18.5%; Score 310; DB 3; Length 10846;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATTATGCTTATTCACCTA 60
Db 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATTATGCTTATTCACCTA 2118
Qy 61 GGCACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGATACAAAGTATGTC 120
Db 2119 GGCACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGATACAAAGTATGTC 2178
Qy 121 CTCCTGTGTTTTAGACATTTATGAATGAACTTTCTTTATGTAATTTTCCAGAACTCCTTGTGTCAG 180
Db 2179 CTCCTGTGTTTTAGACATTTATGAATGAACTTTCTTTATGTAATTTTCCAGAACTCCTTGTGTCAG 2238
Qy 181 ATTCTAATCATGCTTTTATAATTATAGTTATACCTCATGGAATTTGTAGTTAGTATGAAAA 240
Db 2239 ATTCTAATCATGCTTTTATAATTATAGTTATACCTCATGGAATTTGTAGTTAGTATGAAAA 2298
Qy 241 TATTTTTTAATGCAATTTTATGCACTTGCCTGCAATGTTGACACATGCAATGCAATGCACTGC 300
Db 2299 TATTTTTTAATGCAATTTTATGCACTTGCCTGCAATGTTGACACATGCAATGCAATGCACTGC 2358
Qy 301 AGCCACTCGA 310
Db 2359 AGCCACTCGA 2368

RESULT 10
US-09-098-219B-6
Sequence 6, Application US/09098219B
Patent No. 6441277
GENERAL INFORMATION:
APPLICANT: Barry, Gerard
APPLICANT: Cheikh, No. 6441277dine
APPLICANT: Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Biphosphosphate
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: TX
COUNTRY: US
ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/098,219B
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/049,995
FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Kammerer, Patricia A.
REGISTRATION NUMBER: 29,775
REFERENCE/DOCKET NUMBER: MOBT:086
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-787-1400
TELEFAX: 713-787-1440
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 10900 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-09-098-219B-6
Query Match 18.5%; Score 310; DB 3; Length 10900;
Best Local Similarity 100.0%; Pred. No. 2.8e-42;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATTATGCTTATTCACCTA 60
Db 2059 TGACCGAAGTTAATATGAGGAGTAAACACCTTGTAGTTGTACCAATTATGCTTATTCACCTA 2118
Qy 61 GGCACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGATACAAAGTATGTC 120
Db 2119 GGCACAAATATATTTTCAGACCTAGAAAGCTGCAATGTTACTGATACAAAGTATGTC 2178
Qy 121 CTCCTGTGTTTTAGACATTTATGAATGAACTTTCTTTATGTAATTTTCCAGAACTCCTTGTGTCAG 180
Db 2179 CTCCTGTGTTTTAGACATTTATGAATGAACTTTCTTTATGTAATTTTCCAGAACTCCTTGTGTCAG 2238
Qy 181 ATTCTAATCATGCTTTTATAATTATAGTTATACCTCATGGAATTTGTAGTTAGTATGAAAA 240
Db 2239 ATTCTAATCATGCTTTTATAATTATAGTTATACCTCATGGAATTTGTAGTTAGTATGAAAA 2298
Qy 241 TATTTTTTAATGCAATTTTATGCACTTGCCTGCAATGTTGACACATGCAATGCAATGCACTGC 300
Db 2299 TATTTTTTAATGCAATTTTATGCACTTGCCTGCAATGTTGACACATGCAATGCAATGCACTGC 2358
Qy 301 AGCCACTCGA 310
Db 2359 AGCCACTCGA 2368

RESULT 11
US-10-164-204-6
Sequence 6, Application US/10164204
Patent No. 6663906
GENERAL INFORMATION:
APPLICANT: Barry, Gerard
APPLICANT: Cheikh, No. 6663906dine
APPLICANT: Kishore, Ganesh
TITLE OF INVENTION: Expression of Fructose 1,6 Biphosphosphate
FILE REFERENCE: 11899.0086.DVUS02 (MOBT:086-2)
CURRENT APPLICATION NUMBER: US/10/164,204
CURRENT FILING DATE: 2002-06-06
PRIOR APPLICATION NUMBER: 09/098,219
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patent in version 3.1
SEQ ID NO 6
LENGTH: 10900
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: P-FMV/CTP2/Eda/NO3'
US-10-164-204-6

Db 3882 ATTCTAATCATGCTTTTATAATTATAGTATATCTCATGGATTTGTAGTATGAAAA 3941
Qy 241 TATTTTAAATGCAATTTTATGACCTGCAATTTGATTTGACAAATGATC 289
Db 3942 TATTTTAAATGCAATTTTATGACCTGCAATTTGATTTGACAAATGATC 3990

RESULT 14
US-10-015-637-7
; Sequence 7, Application US/10015637
; Patent No. 6927321
; GENERAL INFORMATION:
; APPLICANT: Wang, Qi
; APPLICANT: Dubois, Patrice
; APPLICANT: Liang, Jihong
; APPLICANT: Oulmassov, Tim
; TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof
; FILE REFERENCE: 13587.106
; CURRENT APPLICATION NUMBER: US/10/015.637
; CURRENT FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: US 60/255879
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Pisum sp.
US-10-015-637-7

Query Match 16.8%; Score 282; DB 3; Length 632;
Best Local Similarity 100.0%; Pred. No. 9.9e-38;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGACCGAAGTTAATGACGAGTAACACTTGTAGTTGACCAATTTGCTTATTTCACTA 60
Db 351 TGACCGAAGTTAATGACGAGTAACACTTGTAGTTGACCAATTTGCTTATTTCACTA 410
Qy 61 GGCACAAATATATTTTACAGACCTAGAAAAGCTGCAATGTTACTGAATACAAAGTATGC 120
Db 411 GGCACAAATATATTTTACAGACCTAGAAAAGCTGCAATGTTACTGAATACAAAGTATGC 470
Qy 121 CTCTTGTTGTTTACAGATTTATGAACTTCTCTTATGTAATTTTCCAGAATCTTGTGCAG 180
Db 471 CTCTTGTTGTTTACAGATTTATGAACTTCTCTTATGTAATTTTCCAGAATCTTGTGCAG 530
Qy 181 ATTCTAATCATGCTTTTATTAATTATAGTTATATCTCATGATTTGTAGTTGATGAAAA 240
Db 531 ATTCTAATCATGCTTTTATTAATTATAGTTATATCTCATGATTTGTAGTTGATGAAAA 590
Qy 241 TATTTTAAATGCAATTTTATGACCTGCAATTTGATTTGACAAATGATC 282
Db 591 TATTTTAAATGCAATTTTATGACCTGCAATTTGATTTGACAAATGATC 632

RESULT 15
US-08-549-680A-5
; Sequence 5, Application US/08549680A
; Patent No. 5962768
; GENERAL INFORMATION:
; APPLICANT: CORNELISSEN, MARCUS
; APPLICANT: REYNAERTS, ARLETTE
; APPLICANT: GOSSELE, VERONIQUE
; APPLICANT: VAN AARSEN, ROEL
; TITLE OF INVENTION: MARKER GENE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESS: Birch, Stewart, Kolasch & Birch, LLP
; STREET: P.O. Box 747
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: USA

ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/549,680A
FILING DATE: 16 JANUARY 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30,330
REFERENCE/DOCKET NUMBER: 2121-0111P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEFAX: (703) 205-8050
TELEX: 248345
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7811 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (synthetic)
FEATURE:
NAME/KEY: misc recomb
LOCATION: 1..7811
OTHER INFORMATION: /label= vector ptrVA3
FEATURE:
NAME/KEY: misc feature
LOCATION: 194..218
OTHER INFORMATION: /note= "T-DNA right border"
FEATURE:
NAME/KEY: misc feature
LOCATION: 484..684
OTHER INFORMATION: /note= "the 3' end formation and
OTHER INFORMATION: polyadenylation region of T-DNA gene 7"
FEATURE:
NAME/KEY: CDS
LOCATION: complement (729..1340)
OTHER INFORMATION: /note= "the aac(6') coding
OTHER INFORMATION: sequence"
FEATURE:
NAME/KEY: promoter
LOCATION: 1341..1756
OTHER INFORMATION: /label= 35S promoter
FEATURE:
NAME/KEY: misc feature
LOCATION: 3001..3023
OTHER INFORMATION: /note= "T-DNA left border
OTHER INFORMATION: sequences"
US-08-549-680A-5

Query Match 16.7%; Score 280.2; DB 2; Length 7811;
Best Local Similarity 98.9%; Pred. No. 2.1e-37;
Matches 282; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 319 CTCATCTAAGCCCCCAATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 378
Db 2739 CTCATCTAAGCCCCCAATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATT 2798
Qy 379 AGAATAATTTGTTTATTTGCTTTCCCTATATAAATACGACGATCGTAATTTGCTGTTTAT 438
Db 2799 AGAATAATTTGTTTATTTGCTTTCCCTATATAAATACGACGATCGTAATTTGCTGTTTAT 2858
Qy 439 CAAAATGTACTTTTATTTATATAACGCTGCGGACATCTACATTTTGAATTGAAAAA 498
Db 2859 CAAAATGTACTTTTATTTATATAAATACGCTGCGGACATCTACATTTTGAATTGAAAAA 2918
Qy 499 AATTGGTAATTAATCTTTTCTTTTCTCCATATTGACCATCATCTACTCTGTCATCCATG 558
Db 2919 AATTGGTAATTAATCTTTTCTTTTCTCCATATTGACCATCATCTACTCTGTCATCCATG 2978

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:58:31 ; Search time 1286.41 Seconds
(without alignments)
10767.297 Million cell updates/sec

Title: US-10-541-346-4

Perfect score: 1675

Sequence: 1 tgcacgaagtaatatgag.....tagtgcacacgttggaag 1675

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA Main:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	530.6	31.7	3706	7 US-10-376-763A-6	Sequence 6, Appli
2	530.6	31.7	3778	7 US-10-376-763A-5	Sequence 5, Appli
3	312.8	18.7	7794	10 US-11-057-062-2	Sequence 2, Appli
4	310	18.5	10846	3 US-09-923-109-5	Sequence 5, Appli
5	310	18.5	10846	6 US-10-164-204-5	Sequence 5, Appli
6	310	18.5	10846	7 US-10-705-430-5	Sequence 5, Appli
7	310	18.5	10900	3 US-09-923-109-6	Sequence 6, Appli
8	310	18.5	10900	6 US-10-164-204-6	Sequence 6, Appli
9	310	18.5	10900	7 US-10-705-430-6	Sequence 6, Appli
10	310	18.5	11606	7 US-10-602-475A-9	Sequence 6, Appli
11	295	17.6	11998	9 US-10-477-240-8	Sequence 8, Appli
12	289	17.3	12304	9 US-10-473-945-5	Sequence 5, Appli
13	289	17.3	12497	9 US-10-473-945-4	Sequence 4, Appli
14	282	16.8	632	5 US-10-015-637-7	Sequence 7, Appli
15	282	16.8	632	10 US-11-148-661-7	Sequence 7, Appli
16	280.2	16.7	5365	9 US-10-839-092-57	Sequence 57, Appli
17	280.2	16.7	7713	7 US-10-668-240-6	Sequence 6, Appli
18	280.2	16.7	7794	10 US-11-057-062-2	Sequence 2, Appli
19	280.2	16.7	8179	7 US-10-668-240-5	Sequence 5, Appli
20	280.2	16.7	8296	10 US-11-057-069-1	Sequence 1, Appli
21	280.2	16.7	8590	10 US-11-057-062-1	Sequence 1, Appli
22	280.2	16.7	10249	6 US-10-198-478-14	Sequence 14, Appli
23	280.2	16.7	10312	6 US-10-198-478-15	Sequence 15, Appli

24	280.2	16.7	10339	6 US-10-198-478-13	Sequence 13, Appli
25	278.8	16.6	10603	8 US-10-838-834-26	Sequence 26, Appli
26	278.8	16.6	10078	5 US-10-033-190-3	Sequence 3, Appli
27	271.4	16.2	10575	8 US-10-838-834-24	Sequence 24, Appli
28	271.4	16.2	10677	8 US-10-838-834-25	Sequence 25, Appli
29	271.2	16.2	15490	9 US-10-364-838-1	Sequence 1, Appli
30	246.6	14.7	9382	9 US-10-964-838-2	Sequence 2, Appli
31	245	14.6	562	9 US-10-964-838-8	Sequence 8, Appli
32	245	14.6	15490	9 US-10-964-838-1	Sequence 1, Appli
33	236	14.1	474	7 US-10-415-305-8	Sequence 8, Appli
34	185.8	11.1	792	7 US-10-415-602-15	Sequence 15, Appli
35	154.4	9.2	8056	8 US-10-473-126-386	Sequence 386, App
36	153.4	9.2	4767	8 US-10-838-834-12	Sequence 12, Appli
37	152.6	9.1	3673778	6 US-10-312-841-1	Sequence 1, Appli
38	151.8	9.1	3673778	6 US-10-312-841-1	Sequence 1, Appli
39	151.4	9.0	8056	8 US-10-473-126-386	Sequence 386, App
40	149.4	8.9	158001	7 US-10-211-179-11	GENERAL INFORMATI
41	148.8	8.9	8056	8 US-10-473-126-240	Sequence 240, App
42	146.2	8.7	11978	3 US-09-792-568-8	Sequence 8, Appli
43	146.2	8.7	12438	3 US-09-792-568-8	Sequence 9, Appli
44	145.2	8.7	74665	8 US-10-719-993-6854	Sequence 6854, Ap
45	144.4	8.6	8056	8 US-10-473-126-240	Sequence 240, App

ALIGNMENTS

RESULT 1
US-10-376-763A-6
; Sequence 6, Application US/10376763A
; Publication No. US20040172669A1
; GENERAL INFORMATION:
; APPLICANT: KWS SAAT AG
; TITLE OF INVENTION: Glyphosate tolerant sugar beet
; FILE REFERENCE: KWS-H7-1
; CURRENT APPLICATION NUMBER: US/10/376,763A
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 3706
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: PCR product
US-10-376-763A-6

Query Match	31.7%	Score	530.6;	DB	7;	Length	3706;
Best Local Similarity	92.9%	Pred. No.	1.4e-54;				
Matches	592;	Conservative	0;	Mismatches	9;	Indels	36;
Gaps	2;						
Qy	1	TGACCGAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTGCTTATTCACCTA	60				
Db	3032	TGACCGAGTTAATATGAGGAGTAAACACTTGTAGTTGACCATTTGCTTATTCACCTA	3091				
Qy	61	GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGTGTACTGTAACAAGTAGTGC	120				
Db	3092	GGCAACAATATATTTTCAGACCTAGAAAGCTGCAAAAGTGTACTGTAACAAGTAGTGC	3151				
Qy	121	CTCTGTGTTTTAGACATTTATGAATTTTCTTTATGTATTTTCCAGAAATCCTTTGTGCG	180				
Db	3152	CTCTGTGTTTTAGACATTTATGAATTTTCTTTATGTATTTTCCAGAAATCCTTTGTGCG	3211				
Qy	181	ATTCTAATCATTCCTTTTAAATTTATAGTTATATCTCATGGATTTGTAGTTAGTAAAA	240				
Db	3212	ATTCTAATCATTCCTTTTAAATTTATAGTTATATCTCATGGATTTGTAGTTAGTAAAA	3271				
Qy	241	TATTTTTTAATGCATTTTATGCTTCCCAATTCATTTGACAACATGCATCAATCGACTGC	300				
Db	3272	TATTTTTTAATGCATTTTATGCTTCCCAATTCATTTGACAACATGCATCAATCGACTGC	3331				
Qy	301	AGCCACTCGAGTGG-----	325				

Db 3332 AGCCATCGAGCGGCCCACTCGAGTGGTGGCCGCGATCGTGAAGTTTCTCATCT 3391
|||||
Qy 326 AAGCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 385
|||||
Db 3392 AAGCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 3451
|||||
Qy 386 TTTGTTTATTTGCTTTTCGCTATAAATACGACGGATCGTAATTTGCTGTTTATCAAAATG 445
|||||
Db 3452 TTTGTTTATTTGCTTTTCGCTATAAATACGACGGATCGTAATTTGCTGTTTATCAAAATG 3511
|||||
Qy 446 TACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAATTTGAAAAAAATTTGCT 505
|||||
Db 3512 TACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAATTTGAAAAAAATTTGCT 3570
|||||
Qy 506 AATTACTCTTTCTTTTCCATATTGACATCATACTCATTTGCTGATCAATGATAGATTT 565
|||||
Db 3571 AATTACTCTTTCTTTTCCATATTGACATCATACTCATTTGCTGATCAATGATAGATTT 3630
|||||
Qy 566 CCGGACATGAGCCATTTACAAATTTGAATATATATTA 602
|||||
Db 3631 CCGGACATGAGCCATTTACAAATTTGAATATATATCTTA 3667
|||||

RESULT 2
US-10-376-763A-5
; Sequence 5, Application US/10376763A
; Publication No. US20040172669A1
; GENERAL INFORMATION:
; APPLICANT: KWS SAAT AG
; TITLE OF INVENTION: Glyphosate tolerant sugar beet
; FILE REFERENCE: KWS-H7-1
; CURRENT APPLICATION NUMBER: US/10/376,763A
; CURRENT FILING DATE: 2003-02-28
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 3778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Inserted DNA with 3' and 5' flanking sequences
US-10-376-763A-5

Query Match 31.7%; Score 530.6; DB 7; Length 3778;
Best Local Similarity 92.9%; Pred. No. 1.4e-54;
Matches 592; Conservative 0; Mismatches 9; Indels 36; Gaps 2;
Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 60
Db 3077 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 3136
Qy 61 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGCAATACAAAGTATGTC 120
Db 3137 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGCAATACAAAGTATGTC 3196
Qy 121 CTCCTGTGTTTTAGACATTTATGAACCTTTCTTTATATGTAATTTTCCAGAATCCCTGTCTAG 180
Db 3197 CTCCTGTGTTTTAGACATTTATGAACCTTTCTTTATATGTAATTTTCCAGAATCCCTGTCTAG 3256
Qy 181 ATTCCTAATCATTCCTTTTATGATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 240
Db 3257 ATTCCTAATCATTCCTTTTATGATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 3316
Qy 241 TATTTTAAATGATTTTATGACTTCCCAATTTGACATGCAACATGCAATCAATCGACTGC 300
Db 3317 TATTTTAAATGATTTTATGACTTCCCAATTTGACATGCAACATGCAATCAATCGACTGC 3376
Qy 301 AGCCACTCGAGTGG-----AGGCCTCATCT 325
Db 3377 AGCCACTCGAAGCGGCCCACTCGAGTGGTGGCGCGCATCGATCGTGAAGTTTCTCATCT 3436

Qy 326 AAGCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 385
Db 3437 AAGCCCCATTTGGACGTGAATGTAGACACGTCGAAATAAAGATTTCCGAATTTAGAAATAA 3496
Qy 386 TTTGTTTATTTGCTTTTCGCTATAAATACGACGGATCGTAATTTGCTGTTTATCAAAATG 445
Db 3497 TTTGTTTATTTGCTTTTCGCTATAAATACGACGGATCGTAATTTGCTGTTTATCAAAATG 3556
Qy 446 TACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAATTTGAAAAAAATTTGCT 505
Db 3557 TACTTTTCATTTTATAATAACGCTGCGGACATCTACATTTTGAATTTGAAAAATTTGCT 3615
Qy 506 AATTACTCTTTCTTTTCCATATTGACATCATACTCATTTGCTGATCAATGATAGATTT 565
Db 3616 AATTACTCTTTCTTTTCCATATTGACATCATACTCATTTGCTGATCAATGATAGATTT 3675
Qy 566 CCGGACATGAGCCATTTACAAATTTGAATATATATTA 602
Db 3676 CCGGACATGAGCCATTTACAAATTTGAATATATATCTTA 3712

RESULT 3
US-11-057-062-2/c
; Sequence 2, Application US/11057062
; Publication No. US20050176670A1
; GENERAL INFORMATION:
; APPLICANT: Malvar, Thomas
; APPLICANT: Huang, Shihshieh
; APPLICANT: Luethy, Michael
; TITLE OF INVENTION: Recombinant DNA for Gene Suppression
; FILE REFERENCE: 38-15 (53428)B
; CURRENT APPLICATION NUMBER: US/11/057,062
; CURRENT FILING DATE: 2005-02-10
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 7794
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: recombinant DNA construct in plasmid between Agrobacterium
; OTHER INFORMATION: borders
US-11-057-062-2

Query Match 18.7%; Score 312.8; DB 10; Length 7794;
Best Local Similarity 96.4%; Pred. No. 2.1e-28;
Matches 320; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
Qy 1 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 60
Db 4040 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 3981
Qy 61 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGCAATACAAAGTATGTC 120
Db 3980 GGCACAAATATATTTTCAGACCTAGAAAAGCTGCAAAATGTTTACTGCAATACAAAGTATGTC 3921
Qy 121 CTCCTGTGTTTTAGACATTTATGAACCTTTCTTTATATGTAATTTTCCAGAATCCCTGTCTAG 180
Db 3920 CTCCTGTGTTTTAGACATTTATGAACCTTTCTTTATATGTAATTTTCCAGAATCCCTGTCTAG 3861
Qy 181 ATTCCTAATCATTCCTTTTATGATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 240
Db 3860 ATTCCTAATCATTCCTTTTATGATTTATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 3801
Qy 241 TATTTTAAATGATTTTATGACTTCCCAATTTGACATGCAACATGCAATCAATCGACTGC 300
Db 3800 TATTTTAAATGATTTTATGACTTCCCAATTTGACATGCAACATGCAATCAATCGACTGC 3741
Qy 301 AGCCACTCGAGTGGAGGCTCATCTTAAGCCCC 332
Db 3740 AGCCACTCGAAGCGGCCCTTAATTAAGGCGC 3709

; Sequence 7, Application US/10015637
; Publication No. US20030046727A1

GENERAL INFORMATION:

; APPLICANT: Wang, Qi
; APPLICANT: Dubois, Patrice
; APPLICANT: Liang, Jihong
; APPLICANT: Oulmassov, Tim
; TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof

FILE REFERENCE: 13587.106

CURRENT APPLICATION NUMBER: US/10/015,637

CURRENT FILING DATE: 2001-12-17

PRIOR APPLICATION NUMBER: US 60/255879

PRIOR FILING DATE: 2000-12-18

NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 632

TYPE: DNA

ORGANISM: Pisum sp.

US-10-015-637-7

Query Match

16.8%; Score 282; DB 5; Length 632;

Best Local Similarity 100.0%; Pred. No. 6.5e-25;

Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 60

DB 351 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 410

QY 61 GGCAACAAATATATTTTCAGACCTTAGAAAAGCTGCAAAATGTTTACTGAAATACAAAGTATGTC 120

DB 411 GGCAACAAATATATTTTCAGACCTTAGAAAAGCTGCAAAATGTTTACTGAAATACAAAGTATGTC 470

QY 121 CTCCTGTGTTTTAGACATTTATGAACTTTCCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180

DB 471 CTCCTGTGTTTTAGACATTTATGAACTTTCCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 530

QY 181 ATTCTAATCATTCGTTTATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 240

DB 531 ATTCTAATCATTCGTTTATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 590

QY 241 TATTTTAAATGCAATTTTATGACTTGCCCAATTTGATTGACAAC 282

DB 591 TATTTTAAATGCAATTTTATGACTTGCCCAATTTGATTGACAAC 632

RESULT 15

US-11-148-661-7

; Sequence 7, Application US/11148661

; Publication No. US20050241018A1

GENERAL INFORMATION:

; APPLICANT: Wang, Qi

; APPLICANT: Dubois, Patrice

; APPLICANT: Liang, Jihong

; APPLICANT: Oulmassov, Tim

; TITLE OF INVENTION: Arcelin-5 Promoter and Uses Thereof

; FILE REFERENCE: 13587.106

; CURRENT APPLICATION NUMBER: US/11/148,661

; CURRENT FILING DATE: 2005-06-09

; PRIOR APPLICATION NUMBER: US/10/015,637

; PRIOR FILING DATE: 2001-12-17

; PRIOR APPLICATION NUMBER: US 60/255879

; PRIOR FILING DATE: 2000-12-18

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 7

; LENGTH: 632

; TYPE: DNA

; ORGANISM: Pisum sp.

US-11-148-661-7

Query Match

16.8%; Score 282; DB 10; Length 632;

Best Local Similarity 100.0%; Pred. No. 6.5e-25;

Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 60
DB 351 TGACCGAAGTTAATATGAGGAGTAAACACACTTGTAGTTGTACCATTTATGCTTATTCACCTA 410
QY 61 GGCAACAAATATATTTTCAGACCTTAGAAAAGCTGCAAAATGTTTACTGAAATACAAAGTATGTC 120
DB 411 GGCAACAAATATATTTTCAGACCTTAGAAAAGCTGCAAAATGTTTACTGAAATACAAAGTATGTC 470
QY 121 CTCCTGTGTTTTAGACATTTATGAACTTTCCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 180
DB 471 CTCCTGTGTTTTAGACATTTATGAACTTTCCCTTTATGTAATTTTCCAGAAATCCTTGTGTCAG 530
QY 181 ATTCTAATCATTCGTTTATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 240
DB 531 ATTCTAATCATTCGTTTATATATAGTTATATCTCATGGAATTTGTAGTTGAGTATGAAAA 590
QY 241 TATTTTAAATGCAATTTTATGACTTGCCCAATTTGATTGACAAC 282
DB 591 TATTTTAAATGCAATTTTATGACTTGCCCAATTTGATTGACAAC 632

Search completed: March 31, 2006, 07:57:38

Job time : 1291.41 secs

THIS PAGE LEFT BLANK

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 31, 2006, 06:18:22 ; Search time 99,926 Seconds
(without alignments)
11377.109 Million cell updates/sec

Title: US-10-541-346-2
Perfect score: 20
Sequence: 1 ttgaatatattacaaagc 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	CQ860279 Sequence
2	20	100.0	1675	6	CQ860281 Sequence
3	20	100.0	110000	15	Continuation (140
4	20	100.0	151041	15	AP003258 Oryza sat
5	20	100.0	207782	15	AP003764 Rattus no
6	19	95.0	143780	14	AC130943 Rattus no
7	19	95.0	146469	14	AL355991 Homo sapi
8	19	95.0	170141	14	AL611928 Homo sapi
9	19	95.0	171656	8	AL136380 Human DNA
10	19	95.0	177264	9	AL626782 Mouse DNA
11	19	95.0	215043	14	AC094221 Rattus no
12	19	95.0	225692	14	AC125367 Rattus no
13	19	95.0	281699	14	AC127711 Rattus no
14	18.4	92.0	592	10	BV373314 S21P6596
15	18.4	92.0	606	10	BV595271 S21P6122
16	18.4	92.0	754	10	BV472141 G591P6181
17	18.4	92.0	757	10	BV477181 G591P6408
18	18.4	92.0	761	10	BV484063 S21P6593

19	18.4	92.0	788	10	BV464490
20	18.4	92.0	6649	15	RA535624
21	18.4	92.0	7950	15	AY285674 Raphanus
22	18.4	92.0	8553	6	BD181937
23	18.4	92.0	15654	15	RA535623
24	18.4	92.0	22770	6	CQ815007
25	18.4	92.0	25000	15	RA550021
26	18.4	92.0	30461	8	AF156545
27	18.4	92.0	72477	14	AC135062
28	18.4	92.0	77331	8	AL354983
29	18.4	92.0	101981	8	AC003001
30	18.4	92.0	110000	14	TANN3.08
31	18.4	92.0	127208	8	AL513342
32	18.4	92.0	127476	6	CQ815032
33	18.4	92.0	129422	8	AL589677
34	18.4	92.0	141596	9	AL603923
35	18.4	92.0	143738	8	AC006054
36	18.4	92.0	161447	8	AC023202
37	18.4	92.0	162139	8	AC104235
38	18.4	92.0	162566	8	AC103724
39	18.4	92.0	166538	8	AC078788
40	18.4	92.0	180216	14	AC020726
41	18.4	92.0	184163	14	AC120245
42	18.4	92.0	185775	8	HUMFMRI5
43	18.4	92.0	187799	8	AC062016
44	18.4	92.0	192856	14	AC155623
45	18.4	92.0	193301	8	CNS01DRJ

ALIGNMENTS

RESULT 1
CQ860279
LOCUS CQ860279
DEFINITION Sequence 2 from Patent WO2004072235.
ACCESSION CQ860279
VERSION CQ860279.1
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cerny,R.E., Duong,C., Hart,J.L., Huber,S.A., Krieb,R.L., Listello,J.J., Martens,A.B. and Sammons,B.
TITLE Cotton event mon 88913 and compositions and methods for detection thereof
JOURNAL Patent: WO 2004072235-A 2 26-AUG-2004;
FEATURES Monsanto Technology LLC (US)
Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Chimeric DNA of cotton genomic DNA and transgene insert DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAGC 20
Db 1 TTGAATATATATTACAAAGC 20

RESULT 2
CQ860281
LOCUS CQ860281
DEFINITION Sequence 4 from Patent WO2004072235.
ACCESSION CQ860281
VERSION CQ860281.1
GI:51982087

linear PAT 10-SEP-2004

KEYWORDS .
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
1
AUTHORS Cerny,R.E., Duong,C., Hart,J.L., Huber,S.A., Krieb,R.L.,
Listello,J.J., Martens,A.B. and Sammons,B.
TITLE Cotton event mon 88913 and compositions and methods for
detectionthereof
JOURNAL Patent: WO 2004072235-A 4 26-AUG-2004;
Monsanto Technology LLC (US)
FEATURES Location/Qualifiers
source 1..1675
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Chimeric DNA of cotton genomic DNA and transgene
insert DNA"

ORIGIN
Query Match 100.0%; Score 20; DB 6; Length 1675;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAGC 20
|||||
Db 589 TTGAATATATATTACAAAGC 608
|||||

RESULT 3
AP008207_139
WPCOMMENT

Sequence split into 433 fragments LOCUS AP008207 Accession AP008207

Fragment Name	Begin	End
AP008207_000	1	110000
AP008207_001	100001	210000
AP008207_002	200001	310000
AP008207_003	300001	410000
AP008207_004	400001	510000
AP008207_005	500001	610000
AP008207_006	600001	710000
AP008207_007	700001	810000
AP008207_008	800001	910000
AP008207_009	900001	1010000
AP008207_010	1000001	1110000
AP008207_011	1100001	1210000
AP008207_012	1200001	1310000
AP008207_013	1300001	1410000
AP008207_014	1400001	1510000
AP008207_015	1500001	1610000
AP008207_016	1600001	1710000
AP008207_017	1700001	1810000
AP008207_018	1800001	1910000
AP008207_019	1900001	2010000
AP008207_020	2000001	2110000
AP008207_021	2100001	2210000
AP008207_022	2200001	2310000
AP008207_023	2300001	2410000
AP008207_024	2400001	2510000
AP008207_025	2500001	2610000
AP008207_026	2600001	2710000
AP008207_027	2700001	2810000
AP008207_028	2800001	2910000
AP008207_029	2900001	3010000
AP008207_030	3000001	3110000
AP008207_031	3100001	3210000
AP008207_032	3200001	3310000
AP008207_033	3300001	3410000
AP008207_034	3400001	3510000
AP008207_035	3500001	3610000
AP008207_036	3600001	3710000
AP008207_037	3700001	3810000
AP008207_038	3800001	3910000

AP008207_039	3900001	4010000
AP008207_040	4000001	4110000
AP008207_041	4100001	4210000
AP008207_042	4200001	4310000
AP008207_043	4300001	4410000
AP008207_044	4400001	4510000
AP008207_045	4500001	4610000
AP008207_046	4600001	4710000
AP008207_047	4700001	4810000
AP008207_048	4800001	4910000
AP008207_049	4900001	5010000
AP008207_050	5000001	5110000
AP008207_051	5100001	5210000
AP008207_052	5200001	5310000
AP008207_053	5300001	5410000
AP008207_054	5400001	5510000
AP008207_055	5500001	5610000
AP008207_056	5600001	5710000
AP008207_057	5700001	5810000
AP008207_058	5800001	5910000
AP008207_059	5900001	6010000
AP008207_060	6000001	6110000
AP008207_061	6100001	6210000
AP008207_062	6200001	6310000
AP008207_063	6300001	6410000
AP008207_064	6400001	6510000
AP008207_065	6500001	6610000
AP008207_066	6600001	6710000
AP008207_067	6700001	6810000
AP008207_068	6800001	6910000
AP008207_069	6900001	7010000
AP008207_070	7000001	7110000
AP008207_071	7100001	7210000
AP008207_072	7200001	7310000
AP008207_073	7300001	7410000
AP008207_074	7400001	7510000
AP008207_075	7500001	7610000
AP008207_076	7600001	7710000
AP008207_077	7700001	7810000
AP008207_078	7800001	7910000
AP008207_079	7900001	8010000
AP008207_080	8000001	8110000
AP008207_081	8100001	8210000
AP008207_082	8200001	8310000
AP008207_083	8300001	8410000
AP008207_084	8400001	8510000
AP008207_085	8500001	8610000
AP008207_086	8600001	8710000
AP008207_087	8700001	8810000
AP008207_088	8800001	8910000
AP008207_089	8900001	9010000
AP008207_090	9000001	9110000
AP008207_091	9100001	9210000
AP008207_092	9200001	9310000
AP008207_093	9300001	9410000
AP008207_094	9400001	9510000
AP008207_095	9500001	9610000
AP008207_096	9600001	9710000
AP008207_097	9700001	9810000
AP008207_098	9800001	9910000
AP008207_099	9900001	10010000
AP008207_100	10000001	10110000
AP008207_101	10100001	10210000
AP008207_102	10200001	10310000
AP008207_103	10300001	10410000
AP008207_104	10400001	10510000
AP008207_105	10500001	10610000
AP008207_106	10600001	10710000
AP008207_107	10700001	10810000
AP008207_108	10800001	10910000
AP008207_109	10900001	11010000
AP008207_110	11000001	11110000
AP008207_111	11100001	11210000

AP008207_112 11200001 11310000
AP008207_113 11300001 11410000
AP008207_114 11400001 11510000
AP008207_115 11500001 11610000
AP008207_116 11600001 11710000
AP008207_117 11700001 11810000
AP008207_118 11800001 11910000
AP008207_119 11900001 12010000
AP008207_120 12000001 12110000
AP008207_121 12100001 12210000
AP008207_122 12200001 12310000
AP008207_123 12300001 12410000
AP008207_124 12400001 12510000
AP008207_125 12500001 12610000
AP008207_126 12600001 12710000
AP008207_127 12700001 12810000
AP008207_128 12800001 12910000
AP008207_129 12900001 13010000
AP008207_130 13000001 13110000
AP008207_131 13100001 13210000
AP008207_132 13200001 13310000
AP008207_133 13300001 13410000
AP008207_134 13400001 13510000
AP008207_135 13500001 13610000
AP008207_136 13600001 13710000
AP008207_137 13700001 13810000
AP008207_138 13800001 13910000
AP008207_139 13900001 14010000
AP008207_140 14000001 14110000
AP008207_141 14100001 14210000
AP008207_142 14200001 14310000
AP008207_143 14300001 14410000
AP008207_144 14400001 14510000
AP008207_145 14500001 14610000
AP008207_146 14600001 14710000
AP008207_147 14700001 14810000
AP008207_148 14800001 14910000
AP008207_149 14900001 15010000
AP008207_150 15000001 15110000
AP008207_151 15100001 15210000
AP008207_152 15200001 15310000
AP008207_153 15300001 15410000
AP008207_154 15400001 15510000
AP008207_155 15500001 15610000
AP008207_156 15600001 15710000
AP008207_157 15700001 15810000
AP008207_158 15800001 15910000
AP008207_159 15900001 16010000
AP008207_160 16000001 16110000
AP008207_161 16100001 16210000
AP008207_162 16200001 16310000
AP008207_163 16300001 16410000
AP008207_164 16400001 16510000
AP008207_165 16500001 16610000
AP008207_166 16600001 16710000
AP008207_167 16700001 16810000
AP008207_168 16800001 16910000
AP008207_169 16900001 17010000
AP008207_170 17000001 17110000
AP008207_171 17100001 17210000
AP008207_172 17200001 17310000
AP008207_173 17300001 17410000
AP008207_174 17400001 17510000
AP008207_175 17500001 17610000
AP008207_176 17600001 17710000
AP008207_177 17700001 17810000
AP008207_178 17800001 17910000
AP008207_179 17900001 18010000
AP008207_180 18000001 18110000
AP008207_181 18100001 18210000
AP008207_182 18200001 18310000
AP008207_183 18300001 18410000
AP008207_184 18400001 18510000

AP008207_185 18500001 18610000
AP008207_186 18600001 18710000
AP008207_187 18700001 18810000
AP008207_188 18800001 18910000
AP008207_189 18900001 19010000
AP008207_190 19000001 19110000
AP008207_191 19100001 19210000
AP008207_192 19200001 19310000
AP008207_193 19300001 19410000
AP008207_194 19400001 19510000
AP008207_195 19500001 19610000
AP008207_196 19600001 19710000

Query Match 100.0%; Score 20; DB 15; Length 110000;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTGAATATATATTACAAAGC 20
|||||

Db 27563 TTGAATATATATTACAAAGC 27582
|||||

RESULT 4
AP003258
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
PAC clone:P0463A02.
ACCESSION
AP003258 BA000010
VERSION
AP003258.3 GI:20160658
KEYWORDS
Oryza sativa (japonica cultivar-group)
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1
Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
Katayose, Y., Wu, J., Niimura, Y., Cheng, Z., Nagamura, Y.,
Antonio, B.A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,
Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arica, K.,
Hamada, M., Harada, C., Hijishita, S., Honda, M., Ichikawa, Y.,
Idonuma, A., Iijima, M., Ikeda, M., Ikeda, M., Ito, S., Ito, T., Ito, Y.,
Ito, Y., Iwabuchi, A., Kamiya, K., Karasawa, W., Katagiri, S.,
Kikuta, A., Kobayashi, N., Kono, I., Machita, K., Maehara, T.,
Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,
Nakama, Y., Nakamichi, Y., Nakamura, M., Namiki, N., Negishi, M.,
Ohta, I., Ono, N., Sai, S., Sakai, K., Shibata, M., Shimokawa, T.,
Shomura, A., Song, J., Takazaki, Y., Terasawa, K., Tsuji, K., Waki, K.,
Yanagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukawa, K.,
Zhong, H., Iwama, H., Endo, T., Ito, H., Hahn, J.H., Kim, H.I., Eun, M.Y.,
Yano, M., Jiang, J. and Gojobori, T.
The genome sequence and structure of rice chromosome 1
Nature 420 (6913), 312-316 (2002)
12447438
2 (bases 1 to 151041)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
Submitted (19-FEB-2001) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakia@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
On Apr 16, 2002 this sequence version replaced gi:15146361.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH
(http://www.softberry.com/), GeneMark.hmm
(http://opal.biology.gatech.edu/GeneMark/), GlimmerM
(http://www.tigr.org/tdb/glimmer/glmr form.html), RICEHM
(http://rgp.dna.affrc.go.jp/RiceHM/), SplicePredictor
(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4
(http://globin.cse.psu.edu/html/docs/sim4.html), gap2
(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The
genomic sequence was searched against NCBI NonRedundant Protein

database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at RGP or DDBJ. Protein homologies of the coding regions were searched against NCBI NonRedundant Protein database with BLASTP. ESTs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. and RGP clone ID. Full-length cDNAs represent the identified cDNA sequences using BLASTN with the corresponding DDBJ accession no. A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-' and '-like protein'. A gene without significant homology to any protein but with full-length cDNA or EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein. A gene predicted by two or more gene prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. The orientation of the sequence is from SP6 to T7 of the PAC clone. This sequence of P0463A02 clone has an overlap with B1051E10 (DDBJ: AF003764) clone at 5' end and with B1102E12 (DDBJ: AF003369) clone at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at <http://rgp.dna.affrc.go.jp/GenomeSeq.html>.

FEATURES

source
1..151041
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="1"
/clone="P0463A02"
complement(3771..5470)
/gene="P0463A02.1"
complement(join(<3771..3823,5359..5470))
/gene="P0463A02.1"
/note="start and end point are not identified"
complement(join(3771..3823,5359..5470))
/gene="P0463A02.1"
/note="predicted by GENSCAN etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD52923.1"
/db_xref="GI:5379290"
/translation="MRPLSSELSASSLLSLRPRTNATVTTTSLVLLLEYRWLGG
QTGDDCGDRR"
complement(join(11853..12023,12266..12337))
/gene="P0463A02.2"
complement(join(11853..12023,12266..12337))
/gene="P0463A02.2"
/note="hypothetical ORF
predicted by GENSCAN
this category is not included in IRGSP standard"
complement(join(14289..14531,14841..14912))
/gene="P0463A02.3"
complement(join(14289..14531,14841..14912))
/gene="P0463A02.3"
/note="hypothetical ORF
predicted by GENSCAN
this category is not included in IRGSP standard"
16137..17849
/gene="P0463A02.4"
16137..17849
/gene="P0463A02.4"
/note="supported by full-length cDNA(s): AK071594"
16164..17531
/gene="P0463A02.4"
/note="contains full-length cDNA(s): AK071594"
/codon_start=1
/product="putative benzoyl-CoA:benzyl
alcohol/phenylethanol benzoyltransferase; BPBT"
/protein_id="BAB89606.1"
/db_xref="GI:20160662"

/translation="MAMELSPTVHRRRAVLVGPVSPTPETKRLSDIDQBSLRVHVP
GLIVRGQPPAPCVRDNDGSIIRALSRALVHYVPLAGRLREVEGRKLVDCSGEG
VVFVEADVRLEMEAAAAGHGIRSFPCVDQLVDPVDRSSGGGVSPLVGIQV
TRLLCGGFI VGTAVNHSVCDAMGIVQFLNAVDAAGLPAPAVHATWRELLDARSP
ATAPFHEYDMIDILPGGREADNIVRSFLPSSDIAALKEEALLPHEHRLRGSSST
ATSPVLAALFMRARTAALEVPDADEEVLVAVGFSRIAALGLPSGYGNTLCAYPTTV
MAGELLRGCTGLGDVRLVORAKAAVTAEVYSTAECLVLRRLRLARTNLFVVTDDR
RVGDRVDVFGWGDVYGGPARALFTVSLVNVKSSNVVGAVVSLPSLVMRFRSAELE
SFLNT"
complement(19981..20577)
/gene="P0463A02.5"
complement(<19981..>20577)
/gene="P0463A02.5"
/note="start and end point are not identified"
complement(19981..20577)
/gene="P0463A02.5"
/note="predicted by GENSCAN etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD52924.1"
/db_xref="GI:53792291"
/translation="MRCKCKNICRLNECKEAERCINKFKTHPQERELRGELERAR
ERRAQGRGAHRAAAGALRGRSRQTRAREREPAGSGEVAATMTADAAPVTVGC
GLRSRTQLPFSRVSLTFSFGPTSSRLLAFLRSLRPPRPPQRRRLPSPTRDPPT
PPSPAPSPAPARCLPASPPDRRHALLCTPRDRD"
complement(20727..21140)
/gene="P0463A02.6"
complement(20727..21140)
/gene="P0463A02.6"
/note="hypothetical ORF
predicted by GlimmerM
this category is not included in IRGSP standard"
22720..24042
/gene="P0463A02.7"
22720..24042
/gene="P0463A02.7"
/note="probably inactive due to 3' exon missing in CDS
pseudogene, containing similarity to Zea mays
retrotransposon Opie-2"
/pseudo
25112..28140
/gene="P0463A02.8"
25112..28140
/gene="P0463A02.8"
/note="probably inactive due to including stop codon(s) in
CDS
pseudogene, Opie2a pol"
/pseudo
complement(join(30682..30741,31664..31779,32174..32222))
/gene="P0463A02.9"
complement(join(30682..30741,31664..31779,32174..32222))
/gene="P0463A02.9"
/note="hypothetical ORF
predicted by GENSCAN
this category is not included in IRGSP standard"
36588..38162
/gene="P0463A02.10"
36588..38162
/gene="P0463A02.10"
/note="start and end point are not identified"
36588..38162
/gene="P0463A02.10"
/codon_start=1
/product="putative cytochrome P450"
/protein_id="BAB89608.1"
/db_xref="GI:20160664"
/translation="MEVILLPLVVIITSTMILLIISTAKRHGGTANLPLPPAPPSV
PVVGLLWLRBSNLSPARELHRHGPIILSLTFLSPRAIFVSSREVTHALVQRG
HTFASRPAPAFVALISGCTQTSVSSAPYGLWRSRLRNLTSGVLGHSRAFLYAPARR
WALHLLTDLAAASGNTGGVAVAVDCLQFAMFSLTYMCFGKRLDRRGVREIEAVQ
RELFSYISFQVAFCTVTKRFRWQKVSIRKQEDFLPLIERRKRIKISSM
DNDGSMVCCYVDTIISHKLPEAGDRDLTDGELVSLCTEFLTASVDITVTALQWIMAR
VQEPEIQAKLLDIBINRVWSSDKHEVDEEDIKSMAYLKALVLEGLRRHPPAHFLLSHA

AVEETSLDGHRIIPAGRSVNVSVADVAHDENVMSREEFILPERFLDGGEGAGTDLTGSR
 EIKMPPFGVGRICPGLGALLQLEYFVANNVRFEGMVGMDGCGGINLAERPEFTV
 IMEQLRALVVRRE"
 complement (38560. .41960)
 /gene="P0463A02.11"

Query Match 100.0%; Score 20; DB 15; Length 151041;
 Best Local Similarity 100.0%; Pred. No. 1.6e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTGAATATATATTACAAAGC 20

Db 3308 TTGAATATATATTACAAAGC 3327

RESULT 5

AP003764

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,

BAC clone: B1051E10.

ACCESSION AP003764 BA000010

VERSION AP003764.3 GI:21104808

KEYWORDS

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

REFERENCE

AUTHORS

Sasaki, T., Matsumoto, T., Yamamoto, K., Sakata, K., Baba, T.,
 Katayose, Y., Wu, J., Nimura, Y., Cheng, Z., Nagamura, Y.,
 Antonio, B. A., Kanamori, H., Hosokawa, S., Masukawa, M., Arikawa, K.,
 Chiden, Y., Hayashi, M., Okamoto, M., Ando, T., Aoki, H., Arita, K.,
 Hamada, M., Harada, C., Hijiehta, S., Honda, M., Ichikawa, Y.,
 Idonuma, A., Iijima, M., Ikeda, M., Ikono, M., Ito, S., Ito, T., Ito, Y.,
 Ito, Y., Iwabuchi, A., Kamiya, K., Karasawa, W., Katagiri, S.,
 Kikuta, A., Kobayashi, N., Kono, I., Machita, K., Maehara, T.,
 Mizuno, H., Mizubayashi, T., Mukai, Y., Nagasaki, H., Nakashima, M.,
 Nakama, Y., Nakamichi, Y., Nakamura, M., Namiki, N., Negishi, M.,
 Ohta, I., Ono, N., Saji, S., Sakai, K., Shibata, M., Shimokawa, T.,
 Shomura, A., Song, J. J., Takasaki, Y., Terasawa, K., Tsuji, K., Waki, K.,
 Yamagata, H., Yamane, H., Yoshiki, S., Yoshihara, R., Yukawa, K.,
 Zhong, H., Iwana, H., Endo, T., Ito, H., Hahn, J. H., Kim, H. I., Eun, M. Y.,
 Yano, M., Jiang, J. and Gojobori, T.
 The genome sequence and structure of rice chromosome 1

Nature 420 (6913), 312-316 (2002)

12447438

2 (bases 1 to 207782)

Sasaki, T., Matsumoto, T. and Yamamoto, K.

Direct Submission

Submitted (20-JUN-2001) Takuji Sasaki, National Institute of

Agrbiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,

Tel: 81-298-38-7441, Fax: 81-298-38-7468)

On May 22, 2002 this sequence version replaced gi:14625024.

Genes were predicted from the integrated results of the following:

GENSCAN (http://CCR-081.mit.edu/GENSCAN.html), FGENESH

(http://www.softberry.com/), GeneMark.hmm

(http://opal.biology.gatech.edu/GeneMark/), GlimmerM

(http://www.tigr.org/tdb/glimmer/glmr form.html), RiceHMM

(http://rgp.dna.affrc.go.jp/RiceHMM/), SplicePredictor

(http://bioinformatics.iastate.edu/cgi-bin/sp.cgi), sim4

(http://globin.cse.psu.edu/html/docs/sim4.html), gap2

(http://www.tigr.org/software/glimmer/), BLASTN and BLASTX. The

genomic sequence was searched against NCBI NonRedundant Protein

database, nr (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA

sequence database at RGP or DBJ. Protein homologies of the coding

regions were searched against NCBI NonRedundant Protein database

with BLASTP. ESTs represent the identified cDNA sequences using

BLASTN with the corresponding DBJ accession no. and RGP clone ID.

Full-length cDNAs represent the identified cDNA sequences using

BLASTN with the corresponding DBJ accession no.

A gene with identity or significant homology to a protein is
 classified based on the protein name to indicate the homology level
 such as same name, 'putative-' and '-like protein'. A gene without
 significant homology to any protein but with full-length cDNA or
 EST homology (covering almost the entire length of partial
 sequence) is classified as an 'unknown' protein. A gene predicted
 by two or more gene prediction programs is classified as a
 'hypothetical' protein according to IRGSP standard. A gene
 predicted by a single gene prediction program is also classified as
 a probable 'hypothetical' protein and is included as a
 miscellaneous feature of the sequence.

The orientation of the sequence is from M13rev to -21M13 of the BAC
 clone. This sequence of B1051E10 clone has an overlap with P0440D10
 (DBJ: AP003852) clone at 5' end and with P0463A02 (DBJ: AP003258)
 clone at 3' end. Detailed information on overlap and assembly
 quality together with annotation of this entry is available at
 http://rgp.dna.affrc.go.jp/GenomeSeq.html.

FEATURES

source

1. .207782

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="genomic DNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/chromosome="1"

/clone="B1051E10"

2444. .3621

/gene="B1051E10.1"

join(<2444. .2936, 3029. .>3621)

/note="start and end point are not identified"

join(2444. .2936, 3029. .3621)

/gene="B1051E10.1"

/note="contains EST(s): AU083497 (R3689), AU032203 (R3689)"

/codon_start=1

/product="putative SAG12 protein"

/protein_id="BAB93394.1"

/db_xref="GI:21104809"

/translation="MASSKPLLLGLLSITCLQLVLAANPQPPPPSCDSKDEL
 FMFSOMAKYAKHSCPEQEKRYOVWKGNTNFIGAPRSOTLSCGVGAFAPQTITDS
 VVGNRFGLDSTPEVQQTGFNAGFHSPPPTPLSPHSMOPCCVDMWSGAVTGKVF
 QGNCASWAFASAAIEGLHKIKTVELVSLSEQWVNDCTDSFGSGSGHSDPALNLVA
 SRGCTSSEKYPYTGQSCDVKLLFDHSASVGAFAVPNDERQLALAVARQPTV
 YIDASAQFQYKGVKPCNPGSNHATVIVGVCENFGGEKYIAKNWSNDWGEQ
 GYVLAKDWWPQGTGCLATSPFPFTV"

join(5131. .6135, 18994. .19986)

/gene="B1051E10.2"

join(5131. .6135, 18994. .19986)

/note="probably inactive due to insertion of genes in CDS

/pseudogene, RIM2 protein"

/pseudo

join(7798. .9059, 9459. .11034)

/gene="B1051E10.3"

join(7798. .9059, 9459. .11034)

/gene="B1051E10.3"

/note="putative orf3 of RIRE2"

complement(11679. .14729)

/gene="B1051E10.4"

complement(11679. .14729)

/gene="B1051E10.4"

/note="probably inactive due to no initiation codon in CDS

/pseudogene, polyprotein"

/pseudo

complement(15405. .17171)

/gene="B1051E10.5"

complement(15405. .17171)

/gene="B1051E10.5"

/note="probably inactive due to 5' exon missing in CDS

/pseudogene, GAG-POL precursor"

/pseudo

complement(20778. .21409)

/gene="B1051E10.6"

complement(join(<20778. .20839, 20980. .>21409))

```
/gene="B1051E10.6"
/notes="start and end point are not identified"
complement(join(20776..20839,20980..21409))
/gene="B1051E10.6"
/notes="predicted by FGENSEH etc."
/codon_start=1
/product="hypothetical protein"
/protein_id="BAD53838.1"
/db_xref="GI:53792804"
/translation="MDGRRQTHEGGDGGGGEVEAAVVEMATERVAVGDGPVGEV
KAAGVDPGVGEVGVGGVLDGRTAERTSGGEGVEGGEGGRQRWREGVE
VGVREGGDDGGGGEVEAATERRARRRWRWRGREGSAVTGVCDTGLTVRA
RHR"
gene
  join(21457..21569,22350..22440)
  /gene="B1051E10.7"
  join(21457..21569,22350..22440)
  /gene="B1051E10.7"
  /note="hypothetical ORF
  predicted by GlimmerM
  this category is not included in IRGSP standard"
gene
  join(22943..23072,23161..23208,23291..23895,23973..24434,
  24610..25340,25423..25575,25673..25952,26371..26454,
  26869..26925)
  /gene="B1051E10.8"
  join(22943..23072,23161..23208,23291..23895,23973..24434,
  24610..25340,25423..25575,25673..25952,26371..26454,
  26869..26925)
  /gene="B1051E10.8"
  /note="transposon protein-like"
  complement(28374..28924)
  /gene="B1051E10.9"
  complement(join(<28374..28465,28581..28650,28769..28924))
  /note="start and end point are not identified"
  complement(join(28374..28465,28581..28650,28769..28924))
  /gene="B1051E10.9"
  /note="predicted by GeneMark.hmm etc."
  /codon_start=1
  /product="hypothetical protein"
  /protein_id="BAD53839.1"
  /db_xref="GI:53792805"
  /translation="MATVSOQLGDCGCSAQAGHQRGRRHGRISAVARELVRAVD
  LDPSTQTLCMIVAAATTRFKADNFGPMFIPVDIVGSKLDMEDHLRTSTPIHSSS
  GHY"
gene
  30450..36329
  /gene="B1051E10.10"
  join(30450..30774,31708..31779,31905..31970,32069..32125,
  32219..32286,32370..32451,32747..32802,32947..33249,
  33344..33430,33501..33675,33783..33904,33991..34154,
  34227..34481,34614..34735,34844..34965,35413..35561,
  35648..35786,36017..36329)
  /gene="B1051E10.10"
  /notes="supported by full-length cDNA(s): AK100444"
  join(30666..30774,31708..31779,31905..31970,32069..32125,
  32219..32286,32370..32451,32747..32802,32947..33249,
  33344..33430,33501..33675,33783..33904,33991..34154,
  34227..34481,34614..34735,34844..34965,35413..35561,
  35648..35786,36017..36052)
  /gene="B1051E10.10"
  /note="contains EST(s): AU063400 (C61341), AU085835 (C61341)
  contains full-length cDNA(s): AK100444, AK062168, AK099063"
  /codon_start=1
  /product="putative tetrafunctional protein of glyoxysomal
  fatty acid beta-oxidation"
  /protein_id="BAB93398.1"
  /db_xref="GI:21104813"
  /translation="WAAAAAKGTEMEVGADGVAVITICNPVNSISIDVLLSKEN
  YAEALRRNDVAIVTGGKFGSGFDISSFGVGGKVEQPKVGYISIDITITLEA
  ATKFSVADIGLGGDEVAMACHARIETPAQLGPELQVIGVPGGQRLPRLV
  GLTKALEMLLSKPIKGAHQGLVDSVADLVNTRWALDIDCELPKPIKSLY
  KTDKLEPLGEAREILKFAQAQRQAANLEHPLVICDVIIEEGIVSGFAGLWKEANAF
```

Query Match

100.0%; Score 20; DB 15; Length 207782;

```
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTGAATATATATTACAAGC 20
|||||
Db 87865 TTGAATATATATTACAAGC 87884

RESULT 6
AC130943 143780 bp DNA linear HTG 20-NOV-2002
LOCUS Rattus norvegicus clone CH230-410L18, *** SEQUENCING IN PROGRESS
DEFINITION Rattus norvegicus clone CH230-410L18, ***
AC130943
AC130943.3 GI:25138999
HTG; HTGS PHASE2; HTGS DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM
  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
  Sciurognathi; Muridea; Muridae; Murinae; Rattus.
REFERENCE
  1 (Bases 1 to 143780)
  Muzny,D,Marie., Metzker,M, Lee., Abramzon,S., Adams,C., Alder,J.,
  Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
  Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
  Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
  Biewalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
  Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
  Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
  Chacko,J., Chavez,D., Chen,R., Chen,Y., Chen,Y., Chen,Z., Chu,J.,
  Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
  Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
  Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
  Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
  Egan,A., Escoto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
  Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
  Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
  Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
  Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
  Hollins,B., Howles,S., Hladun,S.L., Hodgson,A., Hogues,M.,
  Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
  Jackson,S., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
  Karpachy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
  Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
  Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
  Lorenshuwa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J.,
  Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
  Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
  Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
  Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
  Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
  Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
  Nwaekemele,O., Okwunolu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
  Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
  Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pul.L., Reigh,R.,
  Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
  Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
  Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
  Sanders,W., Savory,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
  Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajls,D.,
  Sneed,A., Sodergren,B., Song,X.-Z., Sorelle,R., Sosa,J.,
  Steimle,M., Strong,R., Sutton,A., Svatek,A., Taber,P., Taylor,C.,
  Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umami,K.,
  Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
  Wang,O., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
  Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
  Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
  Yu.F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
  Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
  Weinstock,G. and Gibbs,R.A.
  Direct Submission
  Unpublished
  TITLE
  JOURNAL
```


* 1 4659: contig of 4659 bp in length
* 4660 4759: gap of 100 bp
* 4760 10177: contig of 5418 bp in length
* 10178 10277: gap of 100 bp
* 10278 13288: contig of 3351 bp in length
* 13289 13728: gap of 100 bp
* 13729 15928: contig of 2200 bp in length
* 15929 16028: gap of 100 bp
* 16029 21103: contig of 5075 bp in length
* 21104 22003: gap of 100 bp
* 22004 26013: contig of 4810 bp in length
* 26014 26113: gap of 100 bp
* 26114 28336: contig of 2223 bp in length
* 28337 28436: gap of 100 bp
* 28437 31764: contig of 3328 bp in length
* 31765 31864: gap of 100 bp
* 31865 43436: contig of 11572 bp in length
* 43437 43536: gap of 100 bp
* 43537 45726: contig of 2190 bp in length
* 45727 45826: gap of 100 bp
* 45827 49850: contig of 4024 bp in length
* 49851 49950: gap of 100 bp
* 49951 83597: contig of 33647 bp in length
* 83598 83697: gap of 100 bp
* 83698 89161: contig of 5464 bp in length
* 89162 89261: gap of 100 bp
* 89262 92494: contig of 3233 bp in length
* 92495 92594: gap of 100 bp
* 92595 97485: contig of 4891 bp in length
* 97486 97585: gap of 100 bp
* 97586 100084: contig of 2499 bp in length
* 100085 100184: gap of 100 bp
* 100185 112061: contig of 11877 bp in length
* 112062 112161: gap of 100 bp
* 112162 117082: contig of 4921 bp in length
* 117083 117182: gap of 100 bp
* 117183 121364: contig of 4182 bp in length
* 121365 121465: gap of 100 bp
* 121465 125730: contig of 4266 bp in length
* 125731 125831: gap of 100 bp
* 125831 129668: contig of 3838 bp in length
* 129669 129768: gap of 100 bp
* 129769 146469: contig of 16701 bp in length.

FEATURES
source
Location/Qualifiers
1..146469
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/clone_lib="RPC1-11.1"
/clone="RP11-149G23"
1..4659
/note="assembly_fragment:01603
clone_end:SP6
vector_side:left"
4760..10177
/note="assembly_fragment:00298
fragment_chain:1"
10278..13628
/note="assembly_fragment:00832
fragment_chain:1"
13729..15928
/note="assembly_fragment:00657
fragment_chain:1"
16029..21103
/note="assembly_fragment:00451
fragment_chain:1"
21204..26013
/note="assembly_fragment:00964
fragment_chain:1"
26114..28336
/note="assembly_fragment:00715
fragment_chain:2"

misc_feature 28437..31764
/note="assembly_fragment:00592
fragment_chain:2"
31865..43436
/note="assembly_fragment:00602
fragment_chain:2"
43537..45726
/note="assembly_fragment:01102
fragment_chain:3"
45827..49850
/note="assembly_fragment:00532
fragment_chain:3"
49951..83597
/note="assembly_fragment:01625
fragment_chain:3"
83698..89161
/note="assembly_fragment:00330
fragment_chain:4"
89262..92494
/note="assembly_fragment:00141
fragment_chain:4"
92595..97485
/note="assembly_fragment:00934
fragment_chain:5"
97586..100084
/note="assembly_fragment:00611
fragment_chain:5"
100185..112061
/note="assembly_fragment:01069
fragment_chain:6"
112162..117082
/note="assembly_fragment:01346
fragment_chain:6"
117183..121364
/note="assembly_fragment:00110"
121465..125730
/note="assembly_fragment:00294"
125831..129668
/note="assembly_fragment:00955"
129769..146469
/note="assembly_fragment:00166
clone_end:T7
vector_side:right"

ORIGIN
Query Match 95.0%; Score 19; DB 14; Length 146469;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTGAATATATATTACAAAG 19
Db 37702 TTGAATATATATTACAAAG 37720

RESULT 8
LOCUS AL611928 170141 bp DNA linear HTG 16-NOV-2001
DEFINITION Homo sapiens chromosome 1 clone RP11-102H4, 19 unordered pieces.
ACCESSION AL611928
VERSION AL611928.7 GI:16073747
KEYWORDS HTG; HTGS PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Phillimore,B.
TITLE Direct Submission
JOURNAL Submitted (15-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 11, 2001 this sequence version replaced gi:16030263.

(Drosophila), a ribosomal protein S2 (RPS2) pseudogene, the EIF2B3 gene for eukaryotic translation initiation factor 2B subunit 3 gamma 58kDa, a chromosome 14 open reading frame 18 (C14orf18) pseudogene, a peptidylprolyl isomerase A (cyclophilin A) (PP1A) pseudogene, a mitochondrial ribosomal protein S17 (MRPS17) pseudogene and four CpG islands, complete sequence.

ACCESSION

AL136380

VERSION

AL136380.22 GI:19031310

KEYWORDS

HTG; C14orf18; CpG island; EIF2B3; MRPS17; patched; PP1A; PTCH2; RPS2.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

Phillimore, B.

TITLE

Direct Submission

JOURNAL

Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk

COMMENT

Clone requests: clonerequest@sanger.ac.uk
On Feb 28, 2002 this sequence version replaced gi:18857781.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/Chr1>

RPS-88207 is from the library RPCI-5 constructed by the group of Pieter de Jong. For further details see

<http://www.chori.org/bacpac/home.htm>

VECTOR: pCYPAC2

----- Genome Center

Center: Wellcome Trust Sanger Institute

Center code: SC

Web site: <http://www.sanger.ac.uk>

Contact: vegas@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

FEATURES

source

1..171656
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="1"
/map="p33-34.2"
/clone="RPS-88207"
/clone_lib="RPCI-5"

misc_feature

1
/note="Clone left end: RPS-88207"
join(Complement(2001..18541),
complement(AL592166.16:85961..90550))
/gene="PTCH2"

mRNA

/locus_tag="RP11-269F19.8-001"
join(Complement(18339..18541),complement(17325..17517),
complement(7630..7819),complement(7453..7522),
complement(7184..7275),complement(6326..6521),
complement(5387..5508),complement(5092..5239),
complement(4880..5011),complement(4635..4790),
complement(4460..4552),complement(3984..4109),
complement(3774..3892),complement(3321..3669),
complement(2880..3192),complement(2645..2787),
complement(2380..2560),complement(2001..2246),
complement(AL592166.16:90516..90550),

complement(AL592166.16:90278..90415),
complement(AL592166.16:87271..87413),
complement(AL592166.16:87097..87196),
complement(AL592166.16:85961..86697))
/gene="PTCH2"
/locus_tag="RP11-269F19.8-001"
/product="patched homolog 2 (Drosophila)"
/note="match: ESTs: Em:AI853051.1 Em:BE197960.1
Em:BE234509.1 Em:BG384338.1 Em:BI541783.1 Em:BM105989.1
Em:BX634936.1 Em:CD548301.1
match: cDNAs: Em:AF087651.1 Em:AF091501.1 Em:AF119569.1"
join(Complement(18339..18410),complement(17325..17517),
complement(7630..7819),complement(7453..7522),
complement(7184..7275),complement(6326..6521),
complement(5387..5508),complement(5092..5239),
complement(4880..5011),complement(4635..4790),
complement(4460..4552),complement(3984..4109),
complement(3774..3892),complement(3321..3669),
complement(2880..3192),complement(2645..2787),
complement(2380..2560),complement(2001..2246),
complement(AL592166.16:90516..90550),
complement(AL592166.16:90278..90415),
complement(AL592166.16:87271..87413),
complement(AL592166.16:87097..87196),
complement(AL592166.16:86443..86697))
/gene="PTCH2"

/locus_tag="RP11-269F19.8-001"

/standard_name="OTTHUMP00000010158"

/note="match: proteins: Sw:Q9Y6C5"

/codon_start=1

/product="patched homolog 2 (Drosophila)"

/protein_id="CAI23127.1"

/db_xref="GI:56204905"

/db_xref="InterPro:IPR000731"

/db_xref="InterPro:IPR003392"

/db_xref="InterPro:IPR004766"

/translation="MTRSPRLRLPPSYTPPARTAAPQILAGSLKAPLWLRAYFOGLL
FSLGCGIQRHCGKVLFLGLAFLAGLGLMAIETNLEOLWVSGRVSQSLHYTKK
KLGEAAAYTSQMLIQTAQGEENILTEALGLHLQALITASKVQSLYKGSWDLNKK
EQLLEELGPFASLEGPFELDKAQVQAYVGRPCLDLHPCFSPAPNHHSRQAPNVA
HELSGCGFSGFKFMHWQEBLLGGMARDPQGLLRALAEQSLFSSAPNHSRQAPNVA
DYOTD1GWESEQASTVLAQWRFFVOLAQOALPENASQOIHFSS1TD1LHAFSE
VSARVVGCVLLMLAYACTWLRWDCAQSGSVGLAGVLVALAVASGLGICALLGIT
FNAATVLPFLALGIGVDVFLLAHAFTALPCTPQERMGECIGRTGTSVLTSLIN
NMAFLMAALVLPALRAFSLQAIVVGGCTFVAVMLVFPAILSLDLRRHRCQLDLVC
CFSPSCSAQVIQLPQELGDTVPVIAHTLTVAQFTHCEASQHVVTILPQAHLLQ
PPSPDPLGSELFSPGSTRDLGQEEETROKACKLPCARWNLAHFARYQFAPLLQ
SHAKAIVLVLFGLALLGLSLYGATLVQDGLATDVVPRGTKEHFLSAQLRYFSLEYVA
LVTQGGPDYAHQSQRALFDLHQRFSLSKAVLPPPTAQPTWLVHYRNWLOGLIPELFQ
DNASGRITRHSYRNGSEDGALAYKLLIQTGDAQEPDPSQLTTRKLVDRGLIPELF
YMLGTWVSSDDPLGLAASQANFPFPPPEWLHDKYDTTGENLRIPPAQLEPAQPFPL
RGLQKTAQDFVEAIEGARAACAAGAGVHAYPGSPFLFWQYGLGRRCFLAVCILL
VCTPLVCALLLNLPWTAGLIVLVMAMTVELFGIMGFLGKLSAIPVVLVASVGIQV
EFTVHVALGFLTQGSNRNLAHALEHTFAPVTDGASTLGLMLAGSHFDFTVRYF
FAALTVLTLGLLGLVLLPVLLSILGPPPEVIOYKESPEILSPAPQGGSLRWAG
SSLPQSPARVTTSTMTVAHPPLPGAIHPAPDEPPWSPATSSGNLSRRGPGATG"
13103

/note="Clone right end: RP11-269F19"

complement(19399..19560)

/locus_tag="RPS-88207.1-001"

/pseudo

complement(19399..19560)

/locus_tag="RPS-88207.1-001"

/note="match: proteins: Sw:O18789 Sw:P15880 Sw:P27952

Tr:AAGI3953 Tr:AAH02186 Tr:BAB28188 Tr:O55211 Tr:O55212

Tr:O55214 Tr:Q8N5L9"

/pseudo

/codon_start=1

/product="ribosomal protein S2 (RPS2) pseudogene"

/note="match: ribosomal protein S2 (RPS2) pseudogene"

polyA_site

gene

51096..51173,55296..55486,57090..57283..72922,

Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GAFN
Center clone name: CH230-2P14
----- Summary Statistics
Assembly program: Atlas;
Consensus quality: 209974 bases at least Q40
Consensus quality: 211630 bases at least Q30
Consensus quality: 212387 bases at least Q20
Estimated insert size: 224886; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 213195: contig of 213195 bp in length
* 213196 213295: gap of unknown length
* 213296 215043: contig of 1748 bp in length.

FEATURES
source
1. 215043
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clones="CH230-2P14"
213196..213295
/estimated_length=unknown

gap

ORIGIN
Query Match 95.0%; Score 19; DB 14; Length 215043;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGAATATATATACAAAGC 20
|||||
Db 169783 TGAATATATATACAAAGC 169765

RESULT 12
AC125367/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-4F4, WORKING DRAFT SEQUENCE, 5
AC125367
VERSION AC125367.4 GI:30466981
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridea; Muridae; Murinae; Rattus.
1 (bases 1 to 225692)
Muzny,D,Marie., Metzker,M,Les., Abramzon,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Ayagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaraike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Cesar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Daviila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebrgeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hughes,M.,
Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozano,R.J., Lu,X., Ma,J.,
Maheshwari,B., Mahindratne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,B.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwakoelameh,O., Okwuon,G., Olarnpusagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pffannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puzo,M., Quiroz,R., Rachin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savory,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajd,S.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.

Direct Submission
Unpublished
2 (bases 1 to 215043)
Worley,K.C.

Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 215043)

Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:24819444.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuewa, L., Louisedge, H., Lozado, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munday, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwackelmele, O., Okwuonu, G., Olarnpunaagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villanana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wood, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstein, G. and Gibbs, R.A.

Unpublished
Direct Submission
2 (bases 1 to 225692)
Worley, K.C.
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Submitted (24-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 225692)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:22772437.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GAPO
Center clone name: CH230-4F4
----- Summary Statistics

Assembly program: Atlas;
Consensus quality: 212691 bases at least Q40
Consensus quality: 215052 bases at least Q30
Consensus quality: 216903 bases at least Q20
Estimated insert size: 223398; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 218818: contig of 218818 bp in length
* 218819 218918: gap of unknown length
* 218919 220130: contig of 1212 bp in length
* 220131 220230: gap of unknown length
* 220231 221911: contig of 1681 bp in length
* 221912 222011: gap of unknown length
* 222012 223534: contig of 1523 bp in length
* 223535 223634: gap of unknown length
* 223635 225692: contig of 2058 bp in length.
FEATURES
source
1. 225692
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-4F4"
1427. 2267
/note="clone boundary"
clone_end:Sp6
site:ECORI
end_sequence:BH306276"
115825. 117279
/note="wgs contig"
complement(216935..217818)
/note="clone boundary"
clone_end:T7
site:ECORI
end_sequence:BH306274"
218819..218918
/estimated_length=unknown
220131..220230
/estimated_length=unknown
221912..222011
/estimated_length=unknown
223535..223634
/estimated_length=unknown
ORIGIN
Query Match 95.0%; Score 19; DB 14; Length 225692;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TGAATATATATATACAAAGC 20
|||||
DB 87925 TGAATATATATATACAAAGC 87907
RESULT 13
AC127711/c
LOCUS
DEFINITION
Rattus norvegicus clone CH230-62C14, *** SEQUENCING IN PROGRESS
***, 6 unordered pieces.
ACCESSION
AC127711
VERSION
AC127711.3 GI:25078806
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Murinae; Rattus. 1 (bases 1 to 281699)

REFERENCE
AUTHORS

Murny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alabrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biwaio,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregregis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovac,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindaratne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mathiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwackemeoh,O., Okwuonwu,G., Olarunpugoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puzo,M., Quiroz,J., Rachin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,M., Savery,G., Scherer,S., Scott,G., Shatman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL

3 (bases 1 to 281699)

REFERENCE
AUTHORS

Direct Submission
 Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

JOURNAL

On Nov 19, 2002 this sequence version replaced gi:23267553. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold,

individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GZVR
 Center clone name: CH230-62C14
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 235016 bases at least Q40
 Consensus quality: 239978 bases at least Q30
 Consensus quality: 242716 bases at least Q20
 Estimated insert size: 242699; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES	source
gap	8444..8543
misc_feature	8544..9701
misc_feature	25995..261385
gap	261386..261485
gap	262788..262887
gap	265015..265114
gap	268870..268969
ORIGIN	
Query Match	95.0%; Score 19; DB 14; Length 281699;
Best Local Similarity	100.0%; Pred. No. 3.1e+02; Indels 0; Gaps 0;
Matches	19; Conservative 0; Mismatches 0;
Qy	2 TGAATATATATATACAAAGC 20
Db	20568 TGAATATATATATACAAAGC 20550

RESULT 14
 BV373314
 LOCUS
 DEFINITION 592 bp DNA linear STS 28-JAN-2005
 S231P6596FC11.T0 BedlingtonTerrier Canis familiaris STS genomic,
 sequence tagged site.
 ACCESSION BV373314
 VERSION BV373314.1 GI:57627384
 KEYWORDS STS.
 SOURCE Canis familiaris (dog)
 ORGANISM Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.
 REFERENCE 1 (bases 1 to 592)
 AUTHORS Lindblad-Toh, K.
 TITLE The genome sequence of Canis familiaris
 JOURNAL Unpublished (2004)
 COMMENT

Contact: Kerstin Lindblad-Toh
 Whitehead Institute for Biomedical Research, Center for Genome
 Research
 320 Charles Street, Cambridge, MA 02141, USA
 Tel: 6172521477
 Fax: 6172580903
 Email: kersti@genome.wi.mit.edu
 Primer A: No sequence submitted
 Primer B: No sequence submitted
 STS size: 592

Protocol:
 WGS-discovery (WGS):
 Paired-end low-coverage whole genome shotgun reads were generated
 from 9 breeds
 (German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador
 Retriever, English
 Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese
 Water Dog -100,000 each)
 and five other canids (Chinese, Alaskan, Indian and Spanish Gray
 Wolf as well as the
 Californian Coyote).

The WGS reads were placed uniquely on the CanFam1.0 boxer assembly
 and SNP detection was
 carried out by SSAHA-SNP. 863872 reads were annotated as STSs and
 485941 SNPs were
 annotated with alleles from the boxer and the breed or canid from
 which the particular
 read came. The validation rate for these SNPs was estimated at
 approximately 98%.

WGA-discovery (WGA) of Boxer/Poodle SNPs:
 A second set of SNPs was generated using a similar methodology
 except that the contigs
 from the 1.5x poodle assembly (Kirkness 2003) were used instead of
 WGS reads. Since this
 sequence lacked base quality scores, arbitrary quality scores of
 phred 40 were assigned
 before the poodle sequence was placed uniquely on the CanFam1.0
 boxer assembly and SNP
 detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated
 with alleles from the
 boxer and the poodle. The validation rate for these SNPs was
 estimated at approximately TBD%.

Internal-WGA-discovery (I-WGA):
 A third set of SNPs were discovered by comparing reads in the WGA
 assembly. SNPs were
 defined as mismatch positions that had a base quality of >= 30 on
 both reads in a region
 that aligned without gaps, and with at most one additional mismatch
 in the ten flanking
 bases. For each allele, at least one additional read had to confirm
 it. 731476 SNPs were
 annotated with alleles between the two boxer alleles. The
 validation rate for these SNPs

was estimated at approximately TBD%.

FEATURES

Location/Qualifiers
 source

1..592
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="BedlingtonTerrier"
 /db_xref="taxon:9615"
 /map="+" 27 22-544 38436142-38435620"
 /clone_lib="BedlingtonTerrier"
 <1..>592

STS

ORIGIN

Query Match 92.0%; Score 18.4; DB 10; Length 592;
 Best Local Similarity 95.0%; Pred. No. 4.9e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTGAATATATATACAAAGC 20

Db 507 TTGAATCTATATTACAAAGC 526

RESULT 15

BV595271

LOCUS

DEFINITION

BV595271 606 bp DNA linear STS 14-APR-2005
 S215P61223RG4.T0 Clara Pan troglodytes troglodytes STS genomic,
 sequence tagged site.

ACCESSION BV595271

VERSION BV595271.1 GI:62534185

KEYWORDS STS.

SOURCE

ORGANISM

Pan troglodytes troglodytes
 Pan troglodytes troglodytes
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homidae; Pan.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 606)
 Mikelsen, T.S., Hillier, W.L., Eichler, E.E., Zody, M.C. and
 Jaife, D.B.

Initial Sequence of the Chimpanzee Genome and Comparison with the
 Human Genome
 Unpublished (2005)

Contact: Michael C. Zody
 Broad Institute of MIT and Harvard
 320 Charles Street, Cambridge, MA 02141, USA
 Tel: 6172580933

Fax: 6172580930

Email: mczody@broad.mit.edu

Primer A: No sequence submitted

Primer B: No sequence submitted

STS size: 606

Protocol:

23,021,928 chimpanzee whole genome shotgun reads were aligned to
 the Human genome NCBI
 Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors,
 including Clint (Pan

troglodytes verus), 3 other Pan troglodytes verus chimps

(Donald, Karlien, Yvonne), 3 Pan
 troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps
 of unknown origin

(Gon, Unknown Chimp). Common names: Pan troglodytes verus is the
 western chimp and Pan

troglodytes troglodytes is the central chimp. To be included in
 chimpanzee SNP discovery, a

read must be at least 500bp in length, at least 50% of its base
 calls must have Phred

score >= 20, at least 30% of its base calls must satisfy

SNQS (30,25) (single strand NQS, the

base in question has Phred score >= 30, the surrounding 10 bases in
 the read have Phred

score >= 25), and the read must have at least 200 bp SNQS (30,25)
 bases. Reads not uniquely

placed in the genome and read pairs whose two ends were not
 consistently placed were

